

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGGCCGCGCTGGGCTCCTGCCGCTTGTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAAACTTGGCGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTCGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGGCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGGTGCCACATGGGTACCAGGGCCGCTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGGTGCT
GGACGAGGGCGCCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAACCTGTGAGGAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCGAAGACCTGTAATGTGCCGGACTTACCCCTTAAATTATTCAAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGAGAGGCTGC
CTGCTCTCTAACGGTTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGGCCGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGCCATGGCCAACCTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTCAAAATAAGCATTTCCTACTGCATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAATCGCGCAGCACCATGGCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTTAGGTACCTCTGAGGCGGAAGAACCGAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLLPLLLLLPAPPEAAKKPTPCHRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLVCCSPGTYPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEVGWVLDE
GACVDVDECAAEPPPCSAAQFCKNANGSYTCEECDSSCVGCTGEGPNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TG CAC CT CG GT CT AT CG AT TG A AT TCCC CG GG AT CCT CT AG AG AT CC CT C
GAC CT CG ACC CAC CG CT CC CG CAGG CG AGG CG AC CG CCC AG CG CT TAA AC GG A ACA
GCC CT GG CT GAGG GAG CT GAG CG CAG CAG AGT AT CT GAC GG CG CC AG GT TG CG TAG GT CG
GC AC GAG GAG TTT CC CG CAG CG AGG AGG CT GAG CAG CAG AT GG CC CG AGG AG CG CC TT C
CCT CG CC CG CT CG CT GG AGC AT CCT CT GT CG CT GG ACT CG GG CC AGG CG AGG C
CGG CG CC CG CAG GAG GAG GAG CT GT AC CT AT GG AT CG AT GCT CAC CAG GCA AG AG TACT CA
TAGG AT TG AAG AAG AT AT CCT GATT GTT CAG AGG GAA AT GG CAC CT TT AC AC AT GAT
TTCAG AAA AG CG CA AC AG AGA AT GC CAG CT ATT CCT GT CA AT AT CC AT TG A AT TT AC
CT GG CA AG CT GC AGG CG AGG CAG A AT ACT T CT AT GA AT T CCT GT C CT TG CG CT CC CT GG AT A
AAGG CAT CAT GG CAG AT CC AAC CGT CA AT GT CC CT CT GT CG TT GG AA AC AGT GC CT CAC AAGG CA
TCAG TT GT CA AGT GG TTT CC AT GT CT TG GAA AAC AGG AT GG GT GG CAG C AT TT GA AGT
GG AT GT GAT T GT AT GA AT T CT GA AGG CA AC ACC AT T CT CCA AAC AC CT CAA AT GCT AT CT
TCT TAA AAC AT GT CA AC AAG CT GAG T GCC CAGG CG GT GG CAA AT GG AGG CTT TG TA AT
GAA AG AC GC AT CT GCG AGT GT C CT GAT GG GT CC AC GG AC CT C ACT GT GAG AAG CC CTT G
TAC CC CAC GAT GT AT GA AT GG T GACT TT GT GT GACT CCT GG TT CT GC AT CT GCC CAC CT G
GAT T CT AT GG AGT GA ACT GT GAC AA AG CAA ACT GT CT CA ACC AC CT GCT TTA AT GG AGG GAC C
TG TT CT ACC CT GG AAA AT GT AT TT G C CT CC AGG ACT A GAG GAG AG CAG T GT GAA AT CAG
CAA AT G C CC CAC AAC CT GT CG AA AT GG AGG TAA AT G C AT TG GT AAA AGC AA AT GT A AGT GT T
C CAA AG GT TAC CAG GAG AC CT GT T CAA AGC CT GT CG AGC CT GG CT GT GG CAC AT
GGA AC CT G C C AT GA ACC CAA AC AA AT G C CA AT GT CA A G A AG GT TG G C AT GG A AG A C AT G C A A
TAA AAG GT TAC G AAG C CAG C C T C A T A C AT G C C T GAG G C CAG CAG G C C CAG C T CAG G C A G C
AC AC G C C T C A C T TAA AAG G C C GAG G AG C G G C G G G A T C C A C C T G A A T C C A A T T A C A T C T G G
TGA ACT C C G A C AT CT GAA AC GT TT AAG TT AC ACC AAG GT T C AT AG C C T T G T T A A C C T T C A
TGT GT TGA AT GT T CAA A A T A T GT T C AT T A C A C T T A A G A A T A C T G G C C T G A A T T T A T T A G C T
T C A T T A T A A A T C A C T GAG C T G A T A T T A C T C T C C T T T A A G T T T C T A A G T A C G T C T G T A G
C A T G A T G G T A T A G A T T T C T G A T G C T T C A G T G C T T G G A C A G A T T T A T T A T G T C A A T T G A
T C A G G T T A A A A T T T C A G T G T G A T T G G C A G A T A T T T C A A A A T T A C A A T G C A T T T A T G G T
G T C T G G G G G C A G G G G A A C A T C A G A A A G G T T A A A T T G G G C A A A A T G C G T A A G T C A C A A G A A T
T T G G A T G G T C A G T T A A T G T T G A A G T T A C A G C A T T C A G A T T T T A T T G T C A G A T A T T A G A T
G T T T G T T A C A T T T T A A A A T T G C T C T T A A T T T T A A C T C T C A A T A C A A T A T A T T T G A C C
T T A C C A T T A T C C A G A G A T T C A G T A T T A A A A A A A A A T T A C A C T G T G G T A G T G G C A T T T
A A A C A A T A T A A T A T T C T A A A C A C A A T G G A A T A T A T G T A T G A A C T T T T G C A T
T G G C T T G A A G C A A T A T A T A T T G T A A A C A A A C A C A G C T C T T A C C T A A T A A C A T T T T A T
A C T G T T T G T A T G T A A A A T A A A G G T G C T G C T T A G T T T T G G A A A A A A A A A A A A A A A A A
A
C G C C A T G G C C C A A C T G T T A T T G C A G C T T A T A T G

FIGURE 4

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><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
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GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKICGKSCKCSKGYQGDLCSPKVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGCTGGCGTCCGGCGTGCAGAGCCAGGGAGGGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACC**ATG**TGGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGCCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGCGCCGG
GAGCTAGCACCGGGTCTGCACCTGCAGGGCATCCGGACGCGGGAGGCCGGTACTGCCAGGA
GCAGGGACCTGTGCTGCCGCGGCCGTGCGACGACTGTGCCCTGCCCTACCTGGGCCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTCTGATCTA
TCCAGTCTGGAACGTACTGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCTGGAT**GAGGCATTGCTACGCCCTGGCACCA**
TCCGCCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGTGAACCCAGGGGAG
GTGCTTCCCACAGCCTCGAGGCCCTGTGAGAAGTGGCCCAACCTGATTGATGAGCCTCTTGA
CCAAGGCAACTGTGCAGGCTCTGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCCTGTGCGCCCCAGAACCTGCTGTCTGTGAC
ACCCACCAGCAGCAGGGCTGCCCGGTGGCGTCTCGATGGTGCCTGGTGGTCTCGTGC
CCGAGGGGTGGTGTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGGCATGGGACCCACTCAGTCAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCCAACTCCTGGGCC
CAGCCTGGCGAGAGGGCCACTTCCGCATCGTGCAGGGCGTCAATGAGTGCAGATCGAG
AGCTTCGTGCTGGCGTCTGGGCGCGTGGCATGGAGGACATGGGTACTCACTGAGGCTG
CGGGCACACGCCGGGTCCGGCTGGATCCAGGCTAAGGGCGCGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTGCCGACAGAGCCGGGCCAGGCCAGGGCGCTAAT
CCCGCGCGGGTCCGCTGACCGAGCAGGCCCGCCTGGGAGGCCGGCAGGCGAGACTGGCG
GAGCCCCCAGACCTCCCAGTGGGACGGGCGAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGGCCCAACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG
TTGCCAGGTTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTGCACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCACACCTGGC
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT
CCTGGCTCAAGCGGTCCACCTGCCTCCGCCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTTCACTGTTAAAAA
TAAAACCAAAAGTATTGATAAAAAAAA

FIGURE 6

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><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
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ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPPIQGCMHGGRIYPVLGTYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCAAATCCA
ATTCTCTGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCGCCAGG
GNTGGTGTCTGACCACTGCTACCCCTCTGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACGCCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCATCCGCGCAGTTGGCCTCCTGACCCTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCAGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCAGTGGGAGCCTGTCCTGTTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCCTCCAACCCCTCTGTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCAACCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGCCAGGCCTCACATTGTTGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTWARRTSRAVPTCATPAGPMPCSRLPPSLRCSLHSACCSDGPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPFAFSTLNPVLRHLFPOEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCCAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCAACGGCGTCGCATCTCCGCCACGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGGTTCACGGAGATCGTGGAGAACAACTATACGGCCTTCCAGAACGCCGGACGAGG
GCTGGTTCATGGCCTTCACGCCAGGGCGGCCAGGCTCCGCAGCCGCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACGAGAACAGCAGTCGAGTTGGCTCCGCCACCCGCCGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGCTGGGAGGCAGGGCAGCAGCCCTGGCCGCTCCC
CACCCCTTCCCTTAAATCCAAGGACTGGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGCCCGAAGCATCCGAGCCCCAGCTGGGAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTCTGCCGCCCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCTTGCAGACAACCGTCTGGAGGTGGCTGCCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGGAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
CATTTGATTTGCTGTTATTCCCCCTTTTCTTCCACACCACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTCCT
GAAGTCTTGGCTTATCATTCCCTGGGCTCTACTCACAGGTGTCAAACCTCCTGGCCTGCC
CTAGTGTGTGCCGCTCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACCAATTAAATG
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAGAGTTCTCATTGCAGGAAAAC
AAATATTGACACCATTTCACGGGCTGCTTGCCTCAGCTCTGAAGGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTGTCTAAGAACATCACCTGAGCAGTGTGCCTGTTGGCTCTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTATTGTTGACGGGAACCTCCTGACCAACAAAGGTATCGCG
AGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTAATTGCTGTCC
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AAACCACATTCTTGACAGCCTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTGCGGATGCTGACTCAAGGGTTTGATAATCTCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCATTGGTTTGACTGCACTTAAATGGGTACAGAACATGGCTCAA
ATATATCCCTCATCTCTCAAACGTGCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGG
GGATGGCGTCAGGGAATTAAATATGAATCTTGTCCCTGCCCACCACGACCCCCGGCTG
CCTCTTTACCCAGCCCCAAGTACAGCTCTCCGACCCTCAGCCTCCACCCCTCTCTAT
TCCAAACCCTAGCAGAAAGCTACACGCCCTCAAACCTTACCATCGAAACTTCCCACGATT
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CATTGTTGTAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCCTTACCGTGATGGCATA
CAAACTCACATGGGTGAAAATGGGCCACAGTTAGTAGGGGGCATCGTCAGGAGCCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAATTAGAGCCCCGATCCACCTATCGGATT
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CACCAACCATGCCCTCATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGGGGCTGATGGGGGCGCGTGTATATT
GTGCTGGTGGTCTTGCCTAGCGTCTTGTGGCATATGCACAAAAAGGGCGCTACACCTC
CCAGAAGTGGAAATAACACGGGCCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCTGGAGATGACAGAAAACAGTTTCAGATCGTCTCCTAAATAACGAT
CAACTCCTAAAGGAGATTCAAGACTGCAGCCATTACACCCAAATGGGGCATTAATTA
CACAGACTGCCATATCCCCAACAAACATCGGATACTGCAACAGCAGCGTGCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCAGAACATTAGACTCTTGAGAA
CACACTCGTGTGTGCACATAAAGACACCGAGATTACATTGATAATGTTACACAGATGCAT
TTGTGCATTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACTCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKS~~WLI~~ISLGLYSQVS~~KLL~~ACPSVRC~~CDRN~~FVYC~~NERSL~~TSVPLGIP
EGVT~~VLYL~~HNNQINNAGFPAELHN~~VQSVHTV~~YGNQLDEFPMNL~~PKN~~RV~~L~~HQENNIQ~~TI~~
SRAALAQLL~~K~~LEELH~~LD~~DN~~S~~ISTVG~~VEDG~~A~~REA~~ISL~~KLL~~FLSK~~N~~H~~SS~~VPV~~GLP~~P~~V~~DLQ~~EL~~R
VDENRIAV~~I~~SDMAFQ~~NL~~TS~~LER~~L~~I~~VDG~~NLL~~T~~N~~K~~G~~IAEG~~TFS~~H~~L~~T~~K~~KEF~~S~~I~~V~~R~~N~~SL~~H~~PPP~~D~~
LPG~~THL~~I~~R~~LYLQ~~DN~~QINH~~I~~PLTAF~~S~~N~~L~~R~~K~~LER~~L~~DISNNQ~~LR~~MLT~~Q~~GVFD~~N~~LS~~N~~L~~K~~QLT~~A~~R~~NN~~
PWFCDCS~~I~~K~~W~~V~~T~~E~~W~~LY~~I~~P~~S~~SLN~~V~~R~~G~~FC~~M~~C~~Q~~G~~P~~E~~Q~~V~~R~~G~~M~~A~~V~~RE~~L~~N~~M~~N~~L~~SC~~P~~TT~~P~~GL~~P~~L~~F~~TP
APSTASPTTQ~~P~~PTLS~~I~~P~~N~~PS~~R~~S~~Y~~T~~P~~P~~T~~TS~~K~~L~~P~~T~~I~~P~~D~~WD~~G~~R~~E~~R~~V~~T~~P~~P~~I~~S~~E~~R~~I~~Q~~L~~S~~I~~H~~F~~V~~N~~D
TSIQV~~W~~LSL~~F~~TV~~M~~AY~~K~~L~~T~~W~~V~~K~~M~~G~~H~~SL~~V~~GG~~I~~V~~Q~~ER~~I~~V~~S~~GE~~K~~Q~~H~~LS~~V~~N~~L~~E~~P~~R~~S~~TY~~R~~I~~C~~L~~V~~PL
DAF~~N~~YRAVE~~D~~T~~I~~C~~S~~E~~A~~T~~T~~H~~A~~S~~Y~~LN~~N~~GS~~N~~T~~A~~S~~H~~EQ~~T~~TS~~H~~SM~~G~~P~~F~~L~~L~~AG~~L~~IG~~G~~AV~~I~~F~~V~~L~~V~~L
LSVFC~~W~~H~~M~~H~~K~~GR~~Y~~T~~S~~Q~~K~~W~~K~~Y~~N~~R~~G~~R~~R~~K~~D~~D~~C~~E~~A~~G~~T~~K~~K~~D~~N~~S~~I~~L~~E~~M~~T~~E~~T~~S~~F~~Q~~I~~V~~S~~LN~~N~~D~~Q~~L~~L~~K~~G~~
DFRLQ~~P~~I~~Y~~TP~~N~~GG~~I~~NY~~T~~D~~C~~H~~I~~P~~N~~N~~M~~R~~Y~~C~~N~~S~~V~~P~~D~~L~~E~~H~~C~~HT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCGGCGGGAGACAGAGGCAGAGGCAGAGCTGGGCTCCGCTCGCTCCACAGAGCG
ATCCCCGAGGAGAGCGCGGCCCTCGCGAGGCGAAGAGGCCAGAGGAAGACCCGGTGGCTGCGCCCTGCG
TCGCTTCCCAGGCAGGCCGGCTGCAGCCTTGCCTCTTGCCTGAGAAAATGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGGACAGATCGTCTCCTCCCTGCCAGGGCAGGGCAGGGTACAGTGGAGGTCCATCT
CTAGGGCAGACACGCTCGGACCCACCGCAGACGCCCTCTGGAGAGTCTGTGAGAACAGCGGAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATGTTGACA
TCTTGCAATTCTGGACATTGGCTCTGATGTCAACCGAGTGGCCTGCTCAAATATGGCAGCACTGCAAGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCGGATCTGTCACGG
GCACCATGACTGGCTGGCCATCCAGTATGCCCTGAAACATCGCATTCTCAGAACAGCAGAGGGGCCGGCCCTGA
GGGAGAATGTCGACCGGGCTATAATGATCGTACAGATGGGAGACCTCAGGACTCCGTGGCCAGGTGGCTGCTA
AGGCACGGGACACGGCATTCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCACACCTGAAAGTCATTG
GGAGTGAAGCCCATGAGGACCATGTCCTCTGTCAGGCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTCGACGGCCCACATGTGACGACCCCTGGAGCATAACTGTGCCACTTCTGCATCAACATCCCTG
GCTCATACGTCGAGGTGAAACAAAGGCTACATTCTCAACTCGGATCAGACGACTGCGAACATCCAGGATCTGT
GTGCGCATGGAGGACCAACTGTGAGCAGCTGTGTAATGTGCGGGCTCTCGTCTGCCAGTGCTACAGTG
GCTACGGCTGGCTGAGGATGGGAAGAGGTGTGTCGCTGTGAGACTACTGTGCCCTGAGAAAACACCGGATGTGAAC
ATAGTGTGAAATGTCGATGCTCTACCTTGGCTGAGGATTGCTCTTAAACCCAGATGAAAAAA
CGTGCACAAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTAACATGGAGGAGGCT
ACTACTGCGCCTGCCACCGTGGCTACACTCTGGACCCCAATGGCAAAACCTGCAACGGCGAGTGGACCCTGTGAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTAACACGGAGGATTCTCTGTCAGTGCTCAGAAGGTTCC
TCATCAACAGGACCTCAAGACCTGCTCCGGTGGATTACTGCTGCTGAGTGACATGGTTGTGAATACTCT
GTGTCAACATGGACAGATCCTTGCTGCTGAGGACACGTGCTCCGCAAGCGATGGAAAGACGTGTG
CAAAATTGGACTCTGTGCTGGGGGACCCAGGTTGTGAACATTGCTGTAAGCAGTGAAAGATTGTTGTG
GCCAGTGTGAAAGGTTATATACTCCGTGAAGATGGAAAAACCTGCAAGAGAAAGATGTCGCAAGCTATAG
ACCATGGCTGTGAAACACATTGTGTAACAGTGACGACTCATACACGTGCGAGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGAAACGCTGCCAGGAAGGATGTCGCAAATCAACCCACCATGGCTGCAACACATTGTTGTTA
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAGACGGTGCAGAAAT
GCACTGAAGGCCAATTGACCTGGTCTTGTGATCGATGGATCCAAGAGCTTGGAGAAGAGAATTGGAGGTG
TGAAGCAGTTGTCACTGGAAATTAGATTCTGACAATTTCCTTAAAGCCGCTCGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTCACTGAGAAACTTCAACTCAGCAGAACATGAAAAAGCCGTTGGCC
ACATGAAATACATGGAAAGGGCTCTATGACTGGGCTGGCCCTGAAACACATGTTGAGAGAAAGTTTACCAAG
GAGAAGGGCCAGGCCCTTCCACAAGGGTGCAGAGCAGCCATTGTTGCTACCGACGGACGGCTCAGGATG
ACGTCTCCAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTTGCTGAGGAGACTCAGCAGGATCATTG
AGGAGGAACCTACAAGAGATTGCTCTGAGGCCACAAACAGCATTCTTCTATGCCAGACTCAGCAGGATC
ATGAGATAAGTGAAGAAACCTCAAGAAAGGCATCTGTAAGCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACCTGCCAAACGGTCCAACAGCCAACAGAATCTGAGGCCAGTCACTTAAATCTTACGGTCTACACAAAAGCTT
CCTGTTCTAATTTCAGTGCACACAGATATCTGTTGAAGAAGACAATTCTTACGGTCTACACAAAAGCTT
CCCATTCAACAAAACCTCAGGAAGGCCCTTGGAGAAAACAGATCAATGCAAATGAAAACCTTAAATGTT
TCCAGAACCTGCAAACGAAGAAGTAAGAAAATTAAACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCC
TGGAAAATGCGCTGAGATACAGATGAAGATTAGAAATCGCAGCACATTGTTAGTCTATTGTTAGTATCAGGATTCAAT
GAACGCACTGCAAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCCCAGAACAACAGACAAGTATACACTAATTGTTAAATTTCTAGGAAAAAAACCTTAAATGTT
TCAGAATTCTAAGATGAATTACAGGTGAGAATGAATAAGCTATGCAAGGTATTGTTAGTATCAGGATTCAAT
AACTTGCTTCTGCCCTCATCTGCTTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCAAGTCTTACTT
CTGTTAGAACACTGGCCATAGGAAATGCTGTTTTGACTGGACTTACCTGATATATGTTATGGAATGTT
CATAAAATCATAGGACATATGTTACTGAGGAAACAAGTGGATTTTTATACAATATTAAAATCACCACCTCG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFRKSEVERAV
KMRHLSTGTMTGLAIQYALNIAFSEAE GARPLREN VPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAI GVGQVDFN T LKSIGSEPHEDH VFLVANFSQIETLTSV FQKKLCTAHMCSTLEHN
CAHFCINI PGSYVCRCKQGYI LNSDQTT CRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVADYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKP
GCEHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQODHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRS DGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCFCFGYI LREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFR
LAEDGKRCRRKDVKSTHGCEHICVNNNGNSYICKCSEG FVLAEDGRRCKC TEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDS LTISP KAARV GLLQY STQVHTEFTLRFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNHLFYAEDFSTMDEISEKLKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCGGCCAGGGAGGGC
CATGATTCCCTCCGGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCCCTGGGCTGA
GTGCCCTCGCGCCCCCTCGGGGCCAGCTGCAACTGCACTTGCCGCCAACCGGGTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTTCCAGCGTGGTACACCTGCACGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTGCGGCTGGAGGGTCTCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCTGAGCTGCCAGTCTCAAGGAGTAAGCCCCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCGAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTACCTCCGCACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTTGGGTCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTTCCAGTCAGTCTCCAGGC
CCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTTACTGGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTGTTTCAATTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAA

0900 0900 0900 0900 0900 0900

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLLEVSTGPGAA
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCAATGAAACGCCTCCGCTCCTAGGGTTTTCCACTTTG
TTGAATTGTCCTATACTCAAAATTGACCAAGACACCTGCTCTCCAAATGCAAATGTGA
AATAACGCAATGGAATTGAGCCTGCTATTGCAACATGGGATTTCAAGGAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTATCACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAATGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAACTTAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCACTACTGAAATTGTAAAACCGTGAAT
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTTACTGAAATTGTAAAACCGTGAAT
AATTGTCAAAGGGATACATTGTAGTTGGACAAGTTATGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATATTGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTCTAGTCATGAGCTCAAACCC
ACCCACATTATATGAACCTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTTGGAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGTGTAATCACCT
GACACATTTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATT
ACCTCTGGTCTTCAGTCAAATTGAAAGCACCAGGACAACAATTCAAACAAATCTTGCTG
TAGCCTATTCTTGCTGAACTGTTCTTGTGGATCAATACAACAAACTAATAAGCTCT
TCTGTTCAATCATTGCCGGACTGCTACACTACTTCTTTAGCTGCTTGCATGGATGTGC
ATTGAAGGCATACATCTATCTATTGTTGGGTGTCATCTACAACAAAGGGATTGGCA
CAAGAATTGATATCTTGCTATCTAAGCCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTGGCACAACAAAGTATGTTGGCTTAGCACCAGAAACAAACTTATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTTGGCTTGGAGTCAT
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGGAGAAC
TAAGGTCTGTGCAAGAGGGAGCCCTCGCTCTGTTCTCTGGCACCACCTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCCAGGGGATGTTCATTTTATTCCCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGTCCTGTTGGATGTTAAGGTAACATAGAGAATG
GTGGATAATTACAACACTGCACAAAATTTCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCCAATTAACTACTAGACAAAAAGTATTAAATCAGTT
GTTTATGCTATAGGAACGTAGATAATAAGGTTAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTT
CTCAGGAGTGATATCACTGCACCCAAGGAAAGATTCTTCTAACACGAGAAGTATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGTGCCTTGAAACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTGAAAAGGGATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAAACACATTACCATTTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGTTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEVEYRNSVTDLSPTDIITYIEILAESSSSLGYKNNTISAKDTL
SNSTLTFVKTVNNFQRTFVWDLKLSVNRRTHLTLMHTVEQATLRISQSFKQTTEFDT
NSTDIALKVFVFFDSYNMKHIHPHMNMDGYINIIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDYRSLCAF
WNYSPDTMNGSWSSEGCELTYSNETHTSCRCNHLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAICIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSSIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLRSKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGTCCTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTGGGGCCGCTGCGCGGTGGGAGGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCCGCAGATCCGAACGGCCTGGCGGGGTACCCCGGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCCGGGCCGGAGGGGGCTGGGCTGGGCGGAGGCAGG
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
TGTCTTGGGCACCTACCGTGGGCCGTAAGGCCTACTATATAAGGCTGCCGGCCGGAG
CCGCCGCGCCGTCAGAGCAGGAGCGCTCGCTCAGGATCTAGGGCCACGACCATCCAAACCC
GGCACTCACAGCCCCCAGCGCATCCCGTCGCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGGGCGCCCGCTCGCTTCTCGGACGCGGGGCC
CCACGTGCACTACGGCTGGGGCAGCCCCTCCGCCTGCCGCACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTGCGCATCCGTGCCGACGGCGTGTGGACTGCGCGGGGC
CAGAGCGCCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTGCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCCACTCTCTCATTCCTGCCATGCTGCCATGGTCCAGAGGAGGCGTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTCTGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTCAACGGACTGGAGGCCGTGAGGAGTCCAGCTTGTAGAAAGTAAC
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCCGTAGTCCACGTTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCAGTTCTAGCCAATAGACTTGTCTGAT
CATAACATTGTAAGCCTGTAGCTGCCAGCTGCTGCCCTGGCCCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGTCAGTTCTGCTTGAATAACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTTCTCATCACTTC
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTAATTCAAGGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTGGAATTGATCTATCTACTTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGCCACAG
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGACAATTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTGCTGTCCGGTGTACCTGC
TTCCATCTCCAGCCACCAGCCCTCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCCCACCCTTATGTCAACCTGCACTTCTGTTCAAAATCAGGGAAAGAAAAGAT
TTGAAGACCCAAGTCTGTCAATAACTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTCCAACATGATATTATGAGTAATTATTATGTATGTAAGTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHLRPLVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAGAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCTGAATACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAAACTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATTCCCTGTGAAGCCCGAATT
TGTGGATATCGCAGGTGTCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGGCCTTAGTGATTTCCGTTGTGGCCTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAATGTGCAGTGGCTACGCCGTAAATCCCAGCACTTGGAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGCCAATATGGTAAACCC
CATCTCTACTAAAATACAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAAATCACTGAACCCGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAATA
AATAAAACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

FIGURE 24

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT
VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQ
QQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKD
GIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNI
SGIIIAAVVVVA
LVISVCGLGV
CYAQRKGYFSKETSFQKS
NSSSKATTMSENV
QWLTPV
IPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGGCAACATTATTTAACATGCTCCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCCCTGCAAATACTGAAGAAGCATGGGATTAAATATTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAGGAAATAGTAACCTCTTCTCCAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTTCAGTGAAGAAAAACTTGTGTTATGGCATTCA
TTGACAAATGCAAGCATCTCCTTATCAATCAGCTCCTATTGAACTTACTGACTGACTG
TGGAACTCTTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCACTGTGCTACTTGGCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCTTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCCTACAGACTAACATATTGCAAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAACAAACTACTGA
ACTGCTGAAAATGCTGTCCGAUTGAGCAACTTACAAGAACTCTATAATTAACTACA
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGAAAATCCAATTATCAGAATCAAAGACATGAACCTTAAGCCTTATCA
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACAGATAACGCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCATGT
TGCTCTTCAAAGTGTAAATCTCAAATTGGATCTAAATAAAATCCTATTAAAGA
TACGAAGGGGTGATTTAGCAATATGCTACACTAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAGC
TACTAACACCCCTAGATTGTCTTACATTCCCCAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACCTGGTACTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTGACTGTGTCATCCGTTG
GATGAACATGAACAAAACCAACATTGATTGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAGAATGTTGGCAAGTGCATTCAAGGACATGATGAAATTG
CTCCCTTTAGCTCTGAGAGCTTCTTAATCTAAATGTAGAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAAACCTTGCTTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAATGGCGTAACCTCCAAAGAAGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAGAGATATTCAAGGCAATTCACTGGTGTGCTGGAAAGCA
AGTCTAAATCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTATCAGAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTACTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCCTGTATAAACTCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDGPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVVNLKFQFLDNKPNPINRIRRGDFSNMLHLKELGINNMPELISIDSALVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESLMLNSNALSA LYHGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEEPDSLFCVDPPEFQQQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLIDNGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSKASSKILKSSVKWTAFV
KTENSHAAQSARI PSDVKVYNLTHLN PSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLLGIIGVICLISCLSPEMNCDDGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGAGACTCTGGACTTGTCCGACAATGGATTCAAAG
TGTGCACAAAATGCCCTCAATAACCTGAAGGCCAGGGCAGAATTGCCAACACCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAAACATGCTGGCAGACCATTCCCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGGCTGGTTCACTATGGTGTCTCATATGTTGATATTATGAGGCAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATGTGTCCAAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATTGTAAACATTGAA
ACTTGATTTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTC SNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDSL DNR
IQSVHKNAFNNLKARARIANPWHCDCTLQQVLRSMASN HETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGGCCGAG**ATG**CAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCATCCTCTGCTGGTGCT
GGGCTCAGTGTGTCAGGCTGGCCACGGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACCGCCTGCTGGACCTAGGCAAGAACGCATAAAACGCTCAACCAGGACGAGTTGCCAG
CTTCCCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGGAGGCCGAGGCCG
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGTCTCCGAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAAGGACCTGTACAACCTCAAGTCAGTGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCTTCAGCGGCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGGCTGTCCCACCTGCACGGCCT
CATCGTCTGGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTTGGACACCATGACACCCAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCGTCCGCCACCTAGTCTATCTCCGCTTCCCTCAACCTCTCCTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGCAGCTGGCGTGGAGGCCCTATGCCTCCGGCCTCAACTACCTGCGCTGCTCAA
TGTCTCTGGCAACCAAGCTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGTGGTCCGG
CGCCGCTGGGGCTCAACTTCAACCGGCAGCAGCCCACGTGCGCACGCCAGGGAGTTGTCCA
GGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTCACCTGCCCGCG
CCCGCATCCGGACCGAAGGCCAGCAGGTGTTGTGGACGAGGGCCACACGGTGCAGTT
GTGTGCCGGCGATGGCAGCCGCCATCCTCTGGCTCTCACCCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCGACTGCCCATCAGCCAACAA
GACCTTCGCTTCATCTCAACCAGCCGGCAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCTCGACATCAAGACCCCTCATCATGCCACCCATGGCTCATCTCTTC
CTGGCGTCTCTCTGCTGGCTGCTGTTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCCCGCAAGTTCAACATGAAGATGATA**TG**AGGCCGGGGGGGGAGGGACCCCCG
GGCGGCCGGCAGGGGAAGGGCCTGGCGCCACCTGCTCACTCTCAGTCTCCACCTC
CTCCCTACCTCTACACACGTTCTCTTCTCCCTCCGCCCTCCGTCCCCCTGCTGCCCG
CCAGCCCTACCAACCTGCCCTCTTCTACCGAGCTCAGAAGCCCAGACCTGGGACCCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGGCCAGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLLDLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLSVGNQLTLEESVFHSVGNLETLILDSNPLA
CDCRLLWVFRRWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDMSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNLIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCCACCGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCCATCCCCAGCCCCGGGGATTCAAGGCTGCCAGCGCCCAGCC
AGGGAGCCGGCCGGGAAGCGCGATGGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTTCGCCTGCTGCTGGCGCCGGCGGGCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAAACAGTGGTGGCTGGCACCCTGGCTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCACTGGTTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCGTG
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCATTACGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTCTGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGGATGATGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGCCAGAACGCTGTTGCTACACTGTGAGGGTCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCCAACAAAGAGTGAACAGTGGCACCTACGGCTGCACAGCCACCA
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCTCCAGCACCTACCAACGCCATCATCGTGGATCGTGGCTTCATTGTCTTCCGTGCTG
CTCATCATGCTCATCTTCCCTGGCCACTACTTGATCCGGACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCCACAGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGACGACAAGGAATATTCATTAGAGGCCCTGCCACTTCCCTGC
GCCCCCGAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGAGGGAGGAGGGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTGTAAACAAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAACA
AACAAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRIQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIHQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFFFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTTCTCCTTCCTGG
CTTCGGACATTGGAGCACTAAATGAACTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTCTTGTGCGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTACCAATTATTCATGCCAATT
CCTCACTCGACTTTCCCTAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTGCAATGAAATCGTCCGGGGCTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAACAAGATCAAGTCTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGCTTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCCAAGAACAGAGACCTTGCTCCTGGACCCCTGCCAACCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCAGGAACAAACCTTAGCTAAC
GTTTACCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCAGTCCGAAAATCGCACTTGTTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTACATGGATAGCAATTACCTGGACACGGCTGTCCGGGA
GAAATTGGGGCTGCAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACACCTG
CTGAGGTCCCTGCCGTGGACGTGGTCTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCCTTCAAGCAGTGGGCA
GAACGCTTGGGTCGGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTTCTT
TAGAAAGGATTTCATGCTCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGCAGACGGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTCGGTGTTGGTCCGGACTGCTGCTGGT
GTTGTCACCTCCGCCCTCACCGTGGCATGCTCGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCGCTCGAGATTAATTCCCTACAGACAGTCTGT
GACTCTTCTACTGGCACAATGGGCTTACAACCGCAGATGGGCCACAGAGTGTATGACTG
TGGCTCTACTCGCTCTCAGACTTAAGACCCCAACCCAAATAGGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCCT
GACCCCTTACTTAGCTCCCTCCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTTGACAGAAAGCCAGCACGACCCCTGCTGGAG
AACTGACAGTGCCCTCGCCCTCGGCCCCGGGCTGTGGGGTTGGATGCCCGGTTCTATAC
ATATATACATATATCACATCTATATAGAGAGATAGATATCTATTCTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKEICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVLIILNDNLISTLPANVFQYVPITHLDLRG
NRLKTLPYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLAPPQEEETFAPGPLPTPKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGGCSDHIPGSGLKMNCNRRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNALIQLILPGTFNAMPKLRILILMNNLLRSLPVDVFAGVSL
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDIECPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSAAFTVVGMLVFILRNRKRSKRRDANSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGTCGCGGCCCTAAGGAAACTGTTGGC
CGCTGGGCCCGCGGGGGATTCTTGGCAGTTGGGGGTCGTGCGGAGCGAGGGCGAGGGG
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGAGCAGCTCTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCGTCTGCCCTGTGCCTCTGGCAGGCCTCTGGCCGGGCGCTGCTACAGCCTGC
CGCGAACACCCCCACTGCCGACCGTGCTGGCTCGGCCCTGGGGCGCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGCAGGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGGGCGCCAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTGCGACTGGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGGTTCTCCTGGCTGTCCCTCCGACCCCGGGGTCTC
GAAAGCGACACGCTGCAGTGGGTGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGTGGGTGAGGCCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTCAAGTACCAAGTTGAGGTCTTGTGTCCTGCGCCGCCCCGGG
GCCGCCTCTAACTTGAGCTATCGCGGCCCTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGGGACGAAATCGCGCTCGCTGGGACAAACTCTCGGGGATGTGTTGTGTCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAAGCCTAGACGACTTGGGAGG
CTTGCCTGCGAATGTGCTACGGGCTTCAGCTGGGAAGGACGGCGCTTGTGACCA
GTGGGAAGGACAGCCGACCCCTGGGGGACCGGGGTGCCACCAGCGCCGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTTGTCCTGAACAAGACAATTCAAGTAACATCTATTCTGAGATTCTCGATGGGGAT
CACAGAGCACGATGTCTACCCCTCAAATGTCCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAAATTCTACGACTCCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTACGAAAGCCCTCTGCCAGCCA
AGGAAGGAGTCTATGGGCCCGGGCCTGGAGAGTGATCCTGAGCCGCTGCTTGGGCTC
CAGTTCTGACATTGACAAACAAATGGGTGAAAGTCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCCTTGCTGGCGAGTCCCTCTGGCTCTAGTGATGCA**TAGGAAACAGGGGA**
CATGGGCACCTCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACATGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGTACTGGGGACCGGGTAGTGCCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTGGAGAAGTGATTGAACATTCAAGACATTGGAAACAAATAGAACACAATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTGAAATCCCAGGGAAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGL
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPG
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPAALGSSSAHCTNNGVKVGDCDLRDRAGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPGSFKTPNWPDRTDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCAGGTCGCTTCTT
CCTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACTTGGAG
GTGGAAACACTGCCTGGAGGAAGAGAACAGTCAAACAAAGAACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCCCTGGGGAACAGAGAGGCCCTGCCGTGGCTACGGCAGTGTGAAGGAGAACGG
GACACGAGGGGGCAGCGGCACTGTGACTGCCAACGCCGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTCGGTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGGCAATGCAAGAACGG
CTGGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCA
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTCCGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCTGCAGCAGATGTTCTTGGCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTTGGTGTACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCAGTGACCGTGTGGAGGGCTTCATCAAGGGCAGA
TA
ATCGCAGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAGGAA
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT
TCTGTGTTCACCATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPPPKGVLPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGPSCLPCCGGTERPCGGYGQCEGEGRGGSGHCDCQAG
YGEACGQCGLGYFEAERNASHLVCACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKCQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLRSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACTCTGGGTGTTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT
GCCCACCTGGACAGGGCGACATGGAGGAGCTGGCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGGGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTTCGG
CATGGAGCAGCGCTGCCGCCAACAGCGAGCTGGTGAGGCCGTGCTGCCGCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGTGCCCCGCGCAGCGCCGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGGCTCCAACCGCACCTCCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGGAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCCGGAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGCCTCGACAGTGCATGCCCTCGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGCCAGGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGAATTGTGTGTTCTGAAGTGGTACAGGAGAGCTG
GCGATGACTGAACGTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTATTCACTGCACTATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCCANTGTGTCATTGTTACTTGTCCGTAC
TGGATCTGGCTAAAGTCCTCCACCACCACTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAAACACATTTTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPOLEHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCCRQPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCCAGGAGTCCTCGGCGCTGTTGTCAGTGGCCTGATCGCGATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCAGCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGTGGAGTGGAGTTGACCA
AGGAGACACCACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTGCCAAGTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGGCGAACAGCTATGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGTGCCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACCGGAATGGGTATGGACACCCATGACTTCAAATGCTGTGCCATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCACTGGTGTGAGCCTGGTCGGCTACCGCCTATCATCTGCATTGCCCTACT
CAGGTGCTACCGACTCTGGCCCTGATGTCAGTTCACAGGATGCCCTATTGTCCT
TACACCCACAGGGCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGCC
ATCCTCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACCTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTTGGTCTGGCTCTTCTGACTGAC
GACCAGGGCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGCTCTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGTCCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTAAAACGCTGCTCTAAAGAAAAGAAAAGACTGGAGGCTGGCGAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCCGATCACCTGAGGTGGAGTCTGGGATCAGCCTGACCA
ACATGGAGAACCCCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCC
CCAGCTGCTCAGGAGGCCTGGCAACAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSSEQDGSPPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCGCTGTGGGGACAGCATGAGCGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGGCTGGCGCTGCTGCTGCTCGGCCTGGACTAGGCCT
GGAGGCCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTCCCACCCACCAAGTTCCAGTGCCGACCAGTGGCTTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCACTCACGTGGCGTGCACGGCCA
CCCAGACTGTCCCAGCTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACTGCCTATGGGTTATTGCAAGCTGCTGCC
TCAGTGCAAGCCTGGTACCGCCACCCCTCCTCTTGTCTGGCTCGAGCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAC
CTCGCTGCCCTGAGACAAGCAACTGCCACCCAGCTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATCGGGATGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCTGCAAGAATGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGAGCTAGGATGGGAACCTGCCACAGCCAGAAC
GGGCTGGCCCCAGGCAGCTCCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCQKGQCPCPCTGVSDCSGGTDKKL
RNCSRILACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGTCTCGCTCGCGCAGCGCGGGCAGCAGAGGTGGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAGCTGGATGCCCTCTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGTTTCTTGAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAAGTGA
TAATTCCATCTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCTA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTCACTGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTTAAACTT
GATGGGTCTCGTATCTGAGTGCTTACAAAACCTTATCTGGTGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCGTCT
GCCACCCGCCCTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCCCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTCCCCTCATGCTCCGTCTATG
ACGAAGCTGTGAGTGCGGCTTGAGTGCCTAGGCCCCGGTACATGGCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCCCTGCTCGGACAACCTGACATA
ATTGCCAGCAGGAGGGAGGTGGCATCCACCAGCCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGGTTAGACAAATGTAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGGTAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKAGTKRLCLKFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPIQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACCGCGTCCGCTCCGGCCCTCCCCCGCCTCCCGTGCAGGTCGGTCCGGTGGCTAGAGA
TGCTGCTGCCGGTTGCAGTTGCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTGGGGGGCGCACCCGAGTCGGGCCATGAGGCGGGACCGCGTACAGG
CCGTGCTGCCGTGCTGGCTGGGGCTGCCGCCAGGGTCGCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGT
TAAAGTCATTACTTCCATGATACTTCTCGAAGACTGAACCTTGAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGC
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
CACAATTAGGAACCTGGTATGTGGATGAGCCGTCCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTCAACATGAAGAACAAATTTCATTGCAAATATTCTGATGAGAACCCAGCAGTCC
CTAGAGAACGCTGAAGGTGAGGAACAGAGCTGACAACACCTGTACTTCCAGAACAG
GAAGAACGATGCCAAAAAACATTAAAGAAAGTAGAGAACGCTGCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCTTCTCCTCCTGTTGTCACCACAGTTGATGTTGGTT
GGATCTGTAGAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAC
AAGCGAACGCTGACTTAGCTGAGACCCGGCAGACCTGAAGAATATTCAATTCCGAGTGT
CGGGAGAACCCACTCCGATGACATGTTGACTATGACAACATGGCTGTGAACCC
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATT
GTTCTCCCCAGACAAATGGGGAGGAGTAAGGAGTCTGGATGGTGAAAATGAAATAT
GTTATTAGGACATATAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAA
CTCTTATTTCTATAAGGAAATACACAGAACGGTCTATGACAAGCTAGATCAGGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTGGCTGTATC
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAACGGTACCTGCCAGGTCTGG
GAGTCTCAATAATGTCACTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTAC
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACCTGTTCC
CAGCACATATTACACAGAACAGAAATCCAGAATCTTCAAAGCCCACATATGG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSSAPAGIGGPyMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPETQEEAKKTFKESREAALNAYILIPSIPLLLL
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSESGFVTLVSVEGFVTNDIYEFS
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGAGGCACAGCGGTCCCTGCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCC CGGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTTGCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCTACCACCAATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGGGGTGGCCCTGGCGAGCTGCAGGAGGCCATGGCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTGACACGGGGCTGGAGTCCTCTCAAGCC
GCTCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCAAAGTCTGTATCCAACTACCAAAGCTGGAGCCTGA
GGCAGAGAACAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGGATGGCATTGACAGTAGTGATAAAAGTGGACTTCTCATCCTCCT
GGACAAACGTGGCTGCCGAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGCTGGAACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCCTCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCCGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTGACCAAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCAAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCAAGGAAGGAGCAGGTGCCAGAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACGTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAAGTGCCTTATACAAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTTGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGCAGCTGGTGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGACCGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGAACAGAACAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGGCCCTGGCATTGCAAGGGACCGTGGAGTGA
GCACCCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTCTGGCCTTGGGAAAGAACACCTGCAACCAGATGAAGACACGTGGTCG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGACAAGGGCGTATGGGCTCTGTGTGATGACAACGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGCTGGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGGAG
CAGTCCCTGGAGCAGTGCACAGATTGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTAACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACTACATCA
CCACCTTCCTATGTCTCCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCEGRVEEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNWYTVQGTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGCGTCCGGACCGTGGCGGACCGTGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTTCGGCCTTTCCGGCTGCTGCAGTGGTGCAGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGG
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCGCGGCCAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCAAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTGGCTGTTATCTCGAA
CTCTGGCTCTGGCTCTCAGCCTCATGCCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGACTCTGACCAGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGCTCACAAGTGGG
AAAGACTGAAGAAACACATCTGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCAACTTGTGTTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLGCLGVFGLFRLLQWVRGKAYLRNAVVIITGATSGLGKEAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPVLVTFDLTDGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTVDVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAACGCTCGCAGCCACAAAAGGG**ATGAA**TTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGGCACAACTCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA
GGCATTTCCTCGCAATGACGAAGAATAACCATTGCCATTGTCACTGTGGCTCGGCAG
CTGGACATGTCTCGTCCCCTCTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACGGCTGCCCTACAAATAACTGGAGTCAAAACACATG
TCTGTGTCCTAATTCGTAACACTGGCTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTAACACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCA**AT****A**GCACCTAGTTCTGAAAAGTGGACTTACCAAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAACATGTTGAACTCTGTTCTAATTATCCCCATTCTCAATA
TCATTGGCAGGTTGGCAGTCTCATTACTACCACTTGTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTAGAGGTGACTTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATTTTATTGATTGACTTAAATTGTTG
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA
TGAAGGACTATCTAGGGTATTCAACATGAATATCATGAACTCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACCTCACATTCAATGCCAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTTAAAAAAA
AAA
AAAAAAA

FIGURE 58

MKFILLDILLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGI
GRLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKV
KAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGH
IVTVASAAGHVSVFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFI
KNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVK
FDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACCGCGTCCGGACGCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGAGATGGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTGCTCCCTATACAGAAGT
GTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGCAGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAACAGATGCCAGTAGTTCTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGTGGAACATGGGCCTTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTATACAGTGCACTAATTCAAGTTTCCAGATATTCCTGAATATAAAAATA
ATGACTTTATGTCACTGGGGAGTCTTATGCAAGGGAAATATGTGCCAGGCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCAGATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTGGATGAGAAGCAAAAAAGTACTTCCAGAACAGCAGTGCCTGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCAGCTAAC
AAAGTACGCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAAATTGTCACTCCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGAACTATAGTTGAAAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACGCATGGTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTCCATCAGGTAAATTATTC
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGTACATGATTATCGA
TTCATTTATGGAAAAGGATGGATCCTTATGTTGATAAACTACCTCCAAAAGAGAACAT
CAGAGGTTTCATTGCTGAAAAGAAAATCGTAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAAATTATCCTGAAACAAGTGAGC
TTTGTGTTTGGGGAGATGTTACTACAAAATTACATGAGTACATGAGTAAGAATTACA
TTATTTAAAGGATGAAAGGTATGGATGTGACACTGAGACAAAGATGTATAATGA
AATTTAGGGTCTTGAATAGGAAGTTTAATTCTCTAAGAGTAAGTGAAGGAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAACAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGGAAAAGATTCTCAAATGTATAAAAGCTTAGAACAAAAGAACATTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHЛИHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFЕAFEILDKLLGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAALTERSLMGMDWKGSQEYKKAЕKKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTCCGGCTCCGAATGGCACATGTGGATCCCAGTCTTGTGGCTACAACAT
TTTCCTTCTAAACAAGTCTAACAGCTGTTAACAGCTAGTGATCAGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAGCTTCAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGTAGGATAGGAAAGACTGGTTAGTCCTAACATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTAACGGGCCAGAAA
TAGAGATGCTTGTAAAATAAATTTAAAAAAAGCAAGTATTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATCCCTAACATTCCTAACAGAGGGAGAAAGTATGTTAAAATA
GAAAAACAAAATGCAGAAGGGAGGAGACTCACAGAGCTAACACCAGGATAGGGACCCCTGGT
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTTGGTCTGACCACTCTGCCTTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGT
CCTCACGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGCCCTGGAGGTGG
ACAGCGCTCTGGTCTGCTCAGTGGTCTGGGTGCTGGCCCCCAGCAGCCGGC
ATGCCTCAGTTCAGCACCTTCACTCTGAGAATCGTACTGGACCTCAACCACTTGACCGT
CCACCAAGGGACGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCCTCATCGTGAGCCCTGAGCGAAGTGCTCACCTCACCAACAATGTCAACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGGGCTGGATGACCTTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACAGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGGAGA
TGGCAAGCTCTTCACTGGCACGGCTGTGGATGGAAGCAGGATTACTTCCGACCCGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTCGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTTGACAT
CTTCTACATCTACGGCTTGTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGCG
CTCTGCAAGGATGACCCCAAGTCCACTCATCGTGTCCCTGCCCTCGCTGCACCCGGC
CGGGTGGAAATACGCCTCCTGCAGGCTGCTAACCTGGCCAAGCCTGGGACTCACTGGCCC
AGGCCTCAATATCACCAGCCAGGACGATGTACTCTTGCCATCTCCAAAGGGCAGAAG
CAGTATCACCACCCGCCGATGACTCTGCCCTGTGCTGCCCTATCCGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCTGCTACCAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGGAGGACGTCCAGTCACGAAGGGCCTGTCCCCATCGATGATAACTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGCCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGGCTGAAAAAGGTAAGAGTCTATGAGTTAGATGCTCCAATGCC
ATTCACCTCCTCAGCAAAGAGTCCCTTGGAGGGTAGCTATTGGTGGAGATTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGGAGGTAAGAAGGGGTTAATTTGTG
ACTTAGCTCTAGCTACTCCTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCACCAACTTTAAGAAAAACTTTAAGGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTvhQGTGAVYVGAINRV
YKLGTGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLLIIDYSENRLLACGSL
YQGVCKLLRLDDLFI^LVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHSYVSLPGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSA^LCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVKQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFGTKSGKLKKVRVYEFRCSNAI^LLLSKESLLEG^LSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCGGGTCCCCCGCCTAGAGAACACCGATGACCA
CGTGGAGCCTCCGGCGAGGCCGGCCCGCACGCTGGACTCTGCTGCTGGCTCTGGCTCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGGGCTCCGCCATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTTCTGGATCTTCGGGGCTCCATCCACTATTCCTGTCAGGACCTT
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTGAACACCCCTCACCACTATGTCCTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTGGAACCTGGACCTGGAGGCCTCGTCTGATGGCCGAGAGATCG
GGCTGTGGTATTCTCGCTCCAGGCCCTACATCTGAGTGGAGATGGACCTGGGGCTTGCCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCAC
TGATGTCCAGGGTGGTGCACCTCAGTACAAGCGTGGGGACCTATCTGCCGTGCAGGTGGAGAATGAATATG
GTTCCCTATAATAAAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATGGAAACTG
TCCTGACTTCAGACAAACAAGGATGGGCTGAGCAAGGGGATTGTCAGGGAGTCTTGCCACCATCAACTTGCAGT
CAACACACAGGCTGCAGCTACTGACCACCTTCTCTCAACGTCAGGGAGCTCAGGCCAAGATGGTGATGGAGT
ACTGGACGGGTGGTTGACTCGTGGGAGGCCCTCACAAATCTTGGATTCTCTGAGGTTTGAAACACGTGT
CTGCCATTGTGGACGCCGCTCTCCATCAACCTCTACATGTTCCACGGAGGCCAACACTTGGCTCATGAATG
GAGCCATGCACCTCCATGACTACAAGTCAGATGTCACCGACTGACTATGATGTCGTGACAGAAGGCCGCG
ATTACAGGCCAAGTACATGAAGCTCGAGACTCTCGGCTCATCTCAGGCATCCTCTCCCTCCCCAACCTG
ACCTTCTTCCAAAGATGCCGTATGAGCCCTAACGCCAGTCTGTACCTGCTCTGTCGGACGCCCTCAAGTAC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGCATGATGGGGCAGG
TGTTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGTCGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGATCGTGGGGCAGTCACATGGGGAGAATATTGATGACCAGCGCAAAG
GCTTAATTGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGGCTGGACAAATGGNGTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTTGG
TAGCTTGTCCATCAGCTCCAGCCTTGTGACACCTTCTGAGACTGGAGGGCTGGGAGAAGGGGGTTGATTCA
TCAATGCCAGAACCTTGGACGTTACTGGAACATTGGACCCAGAACAGCCTTACCTCCAGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTATCGTTTGAGGAGACGATGGGGCCCTGCATTACAGTCAGGAAACCCCC
ACCTGGGCAGGAACCAAGTACATTAAGTGAAGCGGTGGCACCCCTCTGCTGGTGCAGTGGAGACTGCCCTC
CTCTTGACCTGAAGCCTGGTGGCTGTGCCCCACCCCTACTGCAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTCTGCCCTGTCTCAGCTCAAACCTAAGCCTGAGGAAAGGTGGATGGCTTGGG
TGGCTTGTGATGATGGCTTCTACAGCCCTGCTTGTGCCAGGGCTGTCGGGCTGTCTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACGTCGCCCTTGACCGGACGTACAGCCC
TGCAGGCATCTGCTGGACTCAGCGTGTCTTGTGTTCTGGAGGGCTGGGCCACATCCCTCATGGCCCCCAT
TTTATCCCCGAAATCTGGGTGTGTCACAGTGTAGAGGGTGGGAAGGGGTGTCACCTGAGCTGACTTTGTT
CTTCCCTCACAACCTCTGAGCCTTCTTGGGATTCTGGAAAGGAACCTGGCGTGAAGAACATGTGACTTCCCTT
TCCCTCCACTCGCTGCTTCCACAGGGTGCAGGCTGGGAGAACAGAAATCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGTCCTGGTGTGTCAGTGGAGGAGACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCA
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCA
GGAGGACAGAACGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCCATGTCTGCA
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGGCCGAACAGCAGGGGAGGAGGAGGAGG
GAAGTGTGTCAGTCGCATTGAGCCTTGTCTGGGGCCAGCCAAACACTGGCTTGGCTCACTGTC
GTTGCACTAAAGTATAACCTGAAATCACAA

FIGURE 64

MTTWSLRRR PARTLGLLLL VV LGFLV LRR LDWSTLVPLRLRHRQLGLQAKGWNFM LEDSTFW
IFGGSIHYFRVPREYWRDRLLKMKACGLNTLTTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVII RGPYI CSEMDLGGLPSWLLQDPGMRLRTTYKGFT EAVDLYFDHLM SRV VPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLTSNDNKG DLSKGIVQGV LAT
INLQSTHELQLLTTFLFNVQGTQPKMVMEYWTGFDSWGGPHNILD SSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVTSYDYDAVLTEAGDYTA KYMKL RDFFGSISGIP
LPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGNGQSF GYI LY
TSITSSGILSGH VHD RGQV FVNTV SIGFLDYKTTKIAVPLI QGYTVLRILV ENRG RVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSLSIS
STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTL YLPGPW LSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGCTAGCTAGGTGTAGGGTGGACGGTCCCAGGACC
CTGGTGAGGGTTCTCTACTTGGCCTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAGG
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTACGGTCTGTCGGCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCTGCCTCGTCCCTGCTGCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGTCATGACCGTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTCTGGCAGCCTGCACTACTTCGGTACCGCGGGTGCTTGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCCAACGCCATACAGTTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTGTGCTCGAAAACCTGAATTCAAGAACCTC
AGATCCAGACTTCCTGCCGAGTGGACTCCTGGTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACCTGGCTGGCTCTCCGTGCACTGCTAGG
AGAAAAGATCTTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTGGCCAGCTGACAACATGACCAAAATCTTACCCCTGCTT
CGGAAGTATGAACCCCATGGGCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCGATAAGAAGGGACGCTTCCATTACTACCAAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCCACACCTAACGCTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCTTGGACCTTACCTCCCCGAGCCCAAGATGATGCTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCTAGACTTGCTTGCCTCGGGCCAT
TCATTCAATCTGCCAATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCAAACACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGCTTGGTCTAACAGCAGTGACTCAAGGGCTGTTGAAGCCACCAATTCTG
GGCAAACAATCCTACCCAGTGGATGATGTTCCCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTGTGCAAATGGCCATATCCTCAAGCTCCTCTGGCCCCACATTCT
ACTCCAAACATTCCAATTTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGGTTAACATTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGGAGCCCTAACAAAATTA
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATAACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGTAAAGGTAGGCCGGCATGGCTCATGC
CTGTAATCCAGCAGTGGTAAACCCCGTCTCCACTAAAAAATACAAAATTAGCCGGCGTG
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAAATACAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAACATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLDYWGQNHSTRVSATKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADETLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTTAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTCAGGAAATATT
ACCCACAATATGGCTTACATGTTGAAAAGCTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTTCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGTTAGTGAAAATAACTTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCGATGCTGCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTGAGA
TGCCTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCTGGGTGTATTGCTAAAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTACAAAGTTAGTCATTCAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACAGGAACTGGAT
TTAAAGTCCAATAACATTGCAACATTGAGGAAATCATCAGTTCCAGCATTAAAAGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTATTCTCTAACAAACAAGCTCGAACCTTACCACTGGCAGTATT
AGTTACAGAAACTCAGATGCTAGATGTGAGCTACAACAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGTTGTTG
TGGAAAGATCACCTTTGATAACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGGATTTAAACTAAGATAATATGACACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTAAGTCATTCAATTCAAATCATTGTTTTTCAAGGG
AAAGGAAAGGAAAATTATAATCACTAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKLNRELYLIGNLNSENNKMICLQELSLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCACCGCGTCCGGCCTCTCTGGACTTTGCAATTCCATTCCCTTGACAAACTGACTTTTATTTCT
TTTTTCCATCTCTGGGCAGCTGGGATCCTAGGCGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTTCCCTGACATTGGCATTGCTTAGTGGTGTGGGGAGGGAGACACGTGG
GCTCAGTGCTTGCTGCACATTCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTATTATGCCTGTC
ATCGCTGGTGGTACCTGGGGCTTGCTCTGCTGATAGTGTGCTCTGTCTTACTTCAAAATACACAAAC
GCGCTAAAGCTGCAAAGAACCTGAAGCTGTGGCTGAAAAATACAACCCAGACAAGGTGTGGGCCAAG
AACAGCCAGGCCAAACCAATTGCCACGGAGTCTTGTCTGCCCTGCAGTGCTGTGAAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGTCGACATAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACCTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGCTGGAACAGCTGCTGGAGATCCCTACAGAGAGCTTC
CACTGGGGCAACCTTCAGGAAGGAGTTGGGAGAGAGAACCCACTGTGGGAATGCTGATAAACCAAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGCGGCTTAAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGT
AGAAGGCTCATGCCATTGACCCCTTAATTCTCCTGTTGGCGAGCTGACAATGGCGGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGTGCAATATGGCAGAGACCCACAAGCCATGATCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCAGCTT
GATCCAGATGGAAGCTGAAAGTGAAAACATTAAAGTCTTGACGGAACCTCAGCAATGGCCTGCTAGGG
CAAGTCTCAGTAAAAGACTATGTTCTGTATTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GACTCAGCAAGAATTCAAAGAACCTGCTTGTCTACTACTTCTCTCTTAACATCTTCTATTCCAAACTGTT
GGCGGTTACCTGGATACCTTGGAGGATCCTCACAGCCCCAATTACCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTCGACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTTCAAAGAGATTTCCTAGAAAATAGAC
AAACAGTGCAAATTGATTCTGCCATCTATGATGGCCCTCCACCAACTCTGGCTGATTGGACAAGTCTGT
GGCGGTGTGACTCCCACCTTCAATCGTCAAAACTCTGACTGTCGTTGCTACAGATTGCCAATTCT
TACCGGGGATTCTGCTCTTACACCTCAATTGAGAAACATCAACACTATTTAATTGCTTACTTCAACTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACACTAGAGGCTTTAACTCTAAATGGGAAATACTGCAACTAAA
GACCCAACTTGCAGACAAAATTATAAGTGTGGAATTCTGCTCTTAAATGGATGTGGTACAATCAGA
AAGGTTAGAGATCAGTCATTACTACACCAATAATCACCTTCTGCATCCTCAACTTCTGAAGTGTACCC
CGTCAGAAACAACTCCAGATTGTGAAGTGTGAAATGGACATAATTCTACAGTGGAGATAATACATAACA
GAAGATGATGTAATAACAAAGTCAAATGCACTGGGAAATATAACACCAGCATGGCTTTTGAAATCCAATTCA
TTTGAAGACTATCTGAATCACCATATTATGTGGATTGAACCAAACCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCAAATTGTTGTGTTCTGATACCTGTAGAGCCTCTCCACCTCTGACTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAAGTGCAGATGAAACTTGTGTAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAAATGCCCTTAAATTCTGAGAAGTATGAGCTCTGTGTATCTGAGTGTAAAGTTTGATATGTGAT
AGCAGTGACCACCAGTCTGCTGCAATCAAGGTGTGCTCCAGAACGAGACATTCTTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCAAGTGGCAATTCAAGGATTTCAGCAT
GAAACACATGCCAGAAACTCCAAACCAAGCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTCTG
AATGTGGTGAAGTGTAGCGACAATCACAGTGAGGCATTGTAAATCAACGGGAGACTACAAATACAGAACGCTG
CAGAACTATTAACTAACAGGTCCAACCTAAGTGAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTATGAATAATGAGGAAGGGCTGAAAGTGACACACAGGCCCTGCATGTAACCAAA

FIGURE 70

MELVRRLMPLTLLLISCLAEITMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSIVQLDPDGSCESENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFSPNISIPNCGGYLDTLEGSFTSPNPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCGRTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTIILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVRSKRDISSYKWTDSIIGPIRLKDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTCCCGTTGCTGCTGCTGCTGCTGC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCACCGCCTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGTGGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCCTCGTGCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGAAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTGGACCACTATTACAGAAAATTGTTAATGCCAACCAAGTGGCAGATATTTCAGGC
CTCTGGTCCAATACATTGCTTAACCTCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTCTGGAACTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTTATTCCATAAGCGGAATTTCAG
TTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATACGCCCTGAGGTTCTGTGG
TCGGATGGTGACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTGGCCTGGTT
ATATAATGAAAGCCCAGTTCGGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGTATAACCCAGGACATCTTGTCCA
CATAAATGGGAAAATGCATGACAATAGACAAACTGCTCTGGGCTATAGGAGGAAAGCTGG
AATCTCTGACTATCTAACATTGAAGAATTGGTAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGGCCTGGCTAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGGCCACATCAGGACAGCTGGCCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGGCTGGCTCTAGCCCTAACTATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACACTGGATAAGAAAATTATTGGCAGTTCCAGCCCTTCCCTTCCACTA
AATTTTCTTAAATTACCCATGTAACCATTAACTCTCCAGTGCACCTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACGTGAAAATTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTCTGGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATGAAACATATGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATAATGGTGACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTCTTCTTCAATTATAAACATAAGTGTACTGTAACATTACAAACGTTTAATT
TTTAAAACCTTTGGCTTTGTAATAACACTAGCTAAAACATAAAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIIFLKWPMSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGAGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACACAGGGCTCTGGTCCAAGGCTCTTGCCTGCAGAAAGAGCT
TTCCATCCAGGTGTCATGCAGAATTATGGGGATCACCTTGTGAGCAAAAGCGAACCGAC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCAAACCCAAAGTGTGGAAAATGGGGTGGGTG
TCCTGATTGGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTCATCCAGAAATTATCACCACCAAAAGATCCCCTATTCAACACTCA
AACTGCAACACAAACAGAATTATTGTCAAGTACAGTACCTACTCGGTGGCATCCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTCACAGAAGTTTATGGAAACTAGCACCAGTCTACAGAAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGAGCTGGCTTGAGATTGATTTGC
TATGTCAAAAGGTATGTGAAGGCCTCCCTTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACAAAGTAGTAAAGGAGGAAGGCCAATGATAGCAACCCCTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAAACTACCGTGGCATGCCTGGAA
GCTGAAGTTTAGATGAGACAGAAATGAGGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCTAGCTGGGAAATCAAAGGGCCAAGAACCAAGAACAGTCCACCCCTT
GGTTCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAAC
CCTCTCCTTATTGTAACCTGCTGGATCCTATCCTCTACCTCCAAAGCTTCCCACGGCC
TTCTAGCCTGGCTATGCTCTAAATAATATCCCCTGGAGAAAGGAGTTTGCAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTGAGGCTAGG
TGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAAACACGTATCCACCTGACATGCTCTTGAGCCGGTA
AGAGCAAAAGAATGGCAGAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAGAACAGTAAAGAACAGGCTGAGGATAAGACAGTACACT
GTCAGCAGGGACTGTAACACAGACAGGGTCAAAGTGTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGCTCTACCACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTCTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGGAAGCTATTCTCT
GTTTGATATTCTAGCTTACTCTACCTCCAAACTAATTCTATTCTGAGACTAATCTT
ATTCACTTTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAAGAAC
TACATTGTTACCTCTATACCAAAAGCACATTAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGACAAAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTTTRLLVQGSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNNPKCGKNGGVGLIWKVPVSRQF
AAYCYNSSDTWTNSCIPPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAALKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTGGCACCTCTAATTGCTCTCGTATTGGTGCCGACTTACCGATGG
CTCGCCCAACCTTACTACCTTCTGTGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGCTGCCACCCAACGCGAAGACGTAACCGTGTACTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGAGA
TCCATCACTGTGGAGCAACATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACAGAACGGACAAGAGGGTCACGGATTGTGGAGTTCTTGCCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCCTACCAAGCAACTCCCTACCCGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCATGGACCTCTG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGAGCTCAACCCCCACACAGTGTCAATT
CCAGGCTTTCCATAACCACAAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGAAATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAACGTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTAACTGCTTATC
AGCTATTCAAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTTCTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCCCCAAGGACTCTGCTCCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACCTTGTGCTAGTCCTAAGGAGAACCTTAACCACAAAG
TTTTATCATTGAAGACAATATTGAACAACCCCTATTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCTTGTGGTAGGACTGGAGGAGAAATCCCTGGACTTCAC
TAACCCCTTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRLPPLCHGLPTQREDGNPCDFD
WREVEILMFSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCCTGGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCGGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGTGTGCGTGTCAAATGGTGAAGCT
GTCGGAGAACGGGCCAGAGAAGGACGTGCTGGTGGCCATGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTCACCTGCGGAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGCTTTCTTACCAAGTCCCCA
ACGGGCGCTACCAGTTCAACTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGT
GTGGCCTCTTGAGCAGCTCTCCGGGCTGGAGGAGGGCCTGGACTGGTGCAACCGGG
CTGGCTGCAGGATGCTACGGTCAGTACCCATCATGTTGCCCGGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGGTGTACTACCTGGAGCACCCCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTCTTGCCGCCTGGAAAGTCCATGCCCTGGACCGCTGCGACGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCCTGTGGTCACCGCATCCTAACTGTGGCCCCAGAGCCTGGGT
CCGAAGCTTGGCTTCCCCGACCCGAGAGCCGCTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCGCCGATTCCACTGGCTGTGATTATTGAGTGGTT
CGTTTCCCTGTGGGTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCAAATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGCATTGCGGTTGTGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTTCTCCCTGCC
CAGCCTGGGGAAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCCAGGCAGATCTGAGGAAGGAAGAAACTCCCTCCCCGTTCT
TCCCTCTCGGTTCAAAGAAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLVPLLLLPGSYGLPFYNGFYYNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**AT****G**ATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTCTGGACGGGAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCGAGCTTCGCGCGTGGATCGGCACACGCAGCAGCGGA
CATACGGGACTCGGTGAGCGCGGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACCGGCCGGTGAAGAATTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAGATGCTGGCTGGACGAGCGCGTGGGAGGACAGCC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTCGCACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTATTGCTGAAACCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCGAGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGCTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCT**TG****A**GCACCGCGCACCTGCCACAGCCTCAGAGGCC
CACAATGACCGGAGGGGGCCGCTGGCTGGCCCTCCCTGTCCAGGGCCCCCTGGGTGGCTTC
GCAGATGCAGTCCCAGGCATCCTCCTGCCCTGGCTCTCAGGGACCCCTGGGTGGCTTC
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCAGACCCAGGGACCCCTGGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCACCATAGACTGAAACTCCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGACCTTGAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQQRFFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVVFIDGWPSSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGCACCCGCGCCCCACCAGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCAGTCGGCCAGCGCAACTCGGTCCAGTCG
GGGCGCGGCTGCAGGGCGCAGAGCGGAGATGCAGCGGCTTGGGGCACCCCTGCTGTGCCTGC
TGCTGGCGGGCGGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCAGCCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG
GGTGAGGAACGTATGGAGGACACGCAGCACAAATTGCGCAGCGGGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTACCTCCAGCTAT
ACAATGAGACCAACACAGACAGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGAGCAGAAGGAGCCACGAGTGCATCATCGACGGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGGCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCAGTGGAGACAGCTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCCTGCTGTTCCCTGTGTGCACACCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTCGTGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTGAAGTTGGCAGCTTATGGAGGGTGCAGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCAGTGGGGAGGCTGCCAGGGCT
GCACTGCTGGAGGGAAAGAGATTTAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTAC
TCTTCTTCCAGTAAGTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCA
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGCAGTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTGCCACCCCTGTCAGATTATTGGCTGCTTGCCTCTACCAAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAAATGTGG
AGTCTCCCTCTGATTGGTTGGGAAATGTGAGAAGAGTGCCTGCTTGCCTGAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACGCAGTTCTTCCATGGCATAGGTAAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATT
AGCAGTGTGCTCAGCTTACATGGCTTGATAATTGTTGAGGGAGGAGATGAAACAAAT
CCTCTCTCAGCACAGCCTGGGGAGGGGTATTGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACCAGAGCAGTT
CTGGTTGTGACTCTAAGCTCAGTGCCTCTCCACTACCCACACCCAGCCTGGTGCACCAA
AAGTGTCCCCAAAAGGAAGGAGAATGGATTGTTGAGGCATGCACATCTGGAATTAAG
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGCAGCCGTCCTCTAATGAAGACAAATGATATTGACACTGTCCTCTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGAAACATGGTT
GTAATATGCACTGCGAACACTGAACACTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGATCATCAGAGTCTTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC
ATAAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTAGAAGGACTCTG
AAGATAACAATAATTCTAGCCCATCCACTCTCCTTCCCTCCAAACACACATGTGATGTACACACACATACAC
CACACATACACCTCCCTCCTTCACTGAAGACTCACAGTCACTCACTGTGAGCAGGTCATAGAAAAGGACAC
TAAAGCTTAAGGCAGGCCATTACCTCTGAGCTCCTTGGCTTGTGAGTCACAAAACATGGGAGGG
CCAGGCACGGTACTCACACCTGTAATCCAGCATTTGGGAGACCGAGGTGAGCAGATCACTTGAGGTAGGGAG
TTCGAGACCAGCCTGCCAACATGGAGAAACCCCCATCTACTAAAAATACAAAATTAGCCAGGAGTGGTGGC
AGGTGCTGTAATCCCAGCTACTCAGGTGGCTGAGCCAGGAGATCGCTGAACTCAGGAGGCGGAGGATGCAGT
CAGCTGAGTGCACCGCTGACCTCCAGCCTGGGTGACAGAATGAGACTCTGTCTAACACAAACACGGGAGGA
GGGGTAGATACTGCTTCTCTGCAACCTCTTAACCTGCATCCTCTTCCAGGGCTGCCCTGATGGGCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATAATTGAGGAGGGCAAGAAGTGCAGCCCG
GTGAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGCAAGGGTTGTCGACCCCTAACCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCTTGTGAAATGGTCCCTGCCCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTTGCTAGCTGGGTGGCTGGTGCACACTGCCACTGTGCCCTGGTACCCCTGGCATGTCCTGGCCCCCTCA
GTGTGCTGCCCCAGATCCGGCCCTGGTATACTGCCCTGGCTCCTACCCGAGGCTACACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGACACAGACCCCTGCTCCTGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGGCTACCTGCCAATCTCACAGAGCTGAGCTGCCAGAACAGCTTTCGGA
TGCCCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGGCTGACCTAGAGGAGAACAGCTGACCCGGCT
GGAGGACCACAGCTTGGCAGGGCTGCCAGGCCACTACAGGAACCTATCTCAACCAACACCAGCTTACCGCATCG
CCCCAGGGCTTTCTGCCCTCAGCAACTTGCTGCCCTGACCTCAACTCCAACCTCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAATCTGAGGACTCATGATTGGCGAACAGGTAGATGCCATCCTGACAT
GAACCTTCCGGCCCCCTGGCAACCTGGTGTGGCTAGCAGGATGAACCTGCCGGAGATCTCGGACTATGC
CCTGGAGGGCTGCAAAGCCTGGAGAGCCCTCCTCTATGACAACCAACAGCTGGCCGGGTGCCAGGGGGCACT
GGAACAGGTGCCCCGGCTCAAGTTCCTAGACCTCAACAAGAACCCGCTCAGCGGGTAGGGGGGGGACTTGC
CAACATGCTGCACTTAAAGGAGCTGGGACTGAAACACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT
GAACCTCCCCGAGGTGACCAAGCTGGACATCACCAATAACCCACGGCTGCTTCCATCCACCCCCGGCCTTCCA
CCACCTGCCCCAGATGGAGACCCCTATGCTCAACAAACAGCTCTCAGTGCCTGCACCAGCAGACGGTGAGTC
CCTGCCAACCTGCAAGGAGGTAGGTCTCCAGGCAACCCATCCGCTGTACTGTGTCATCCGTTGGCCAATGC
CACGGGCAACCGTGTGGCTCATGAGCCGAATCCACCCCTGTCGCGAGCCTCCAGCGCCTCC
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGGACTGTGTTGCCCTCATCTCCCCACGAAGCTCCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGGAGCATGGTGTGCAATTGCCGGCACTGCCGAACCGAACCAGGAGATCTACTG
GGTCACCTCAGCTGGCTTCACTGACACCTGCCATGCAAGGAGGTACCGGGGTGACCCCGAGGGGACCC
GGAGCTCGGGAGGGTACAGCAGAAGAGGAGGGCTATAACACTGTGTCGCCCCAGAACCTGGGGGCTGACAC
TAAGACGGTTAGTGTGGTGTGGCCGTGCTCTCCAGGCCAGGGAGCAAGGGACAGGGGCTGGAGCTCCG
GGTGCAGGAGACCACCCCTATCACATCTGCTATCTGGTCAACCCACCAACACAGTGTCCACCAACCTC
CTGGTCACTGCTGCCCTCCCTCCGGGGCCAGGGGCCACAGCTCTGCCCGCCTGCCTGGGGAAACCCACAGCTA
CAACATTACCCGCCCTCTCAGGCCACGGAGTACTGGGCTCTCCAGGCCAGGGAGCAAGGGACAGGGGCTGGAGCTCCG
GTGTTGGCTTGTGTGGCCAGACAAAGAGGCCACTTCTGGCACAGAGCCTTAGGGGATGTCCTGGGCTCAT
TGCCTCTGGCTCTGGCTGCTCTCTCTGGCAGCTGGCTAGCGGCCACCTTGGCACAGGCCACCCAGGAA
GGGTGTGGGTGGGAGGGGGCTCTCCCTCCAGGCTGGCTTCTGGGCTGGAGTGCCTTCTGTGTCGGGGTTGT
GTCTGCTCCCTCGTCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCTCAGAACAGGGGAGACACTGTTGCC
ACCATTGTCTCAAATTCTTAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAA
AGAGAACAGCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTGAGGCCCTGGCAGCTGGG
CAAGACAGATGGGCTTGTGGCCCTCTGGGGTGCTTCTGCAGCCTTGAAGGAAAGTGGCCCTTACCTCTAGGGTCA
CCTCTGCTGCCATTCTGAGGAACATCTCAAGGAACAGGAGGGACTTGGCTAGGCCCTCTGCCCTCCCCATCTT
CTCTCTGCCAGAGGCTCTGGGCTGGCTTGTGTCCTGGCACAGGCCAGATCTGACTTCTACCTGTGTCCTGGGCTGC
TCTTCTCTGTCAGTCTCAGTTGCTTGTGTCCTGGCACAGGCCAGGCTGAAGGAGGCAACTCCATCTCAC
CTCGGGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTGGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGAGAA
ATGTGTCACCTCCCCAACCCGATTCACTCTTCTCTGTTGAAAAAATAAAAATAAAACAATAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLQLQSNSIVRVDQSELGYLANLTELDSQNSFSDARDCDFHALPQLLSSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMMNFRPLANLRLSLVLAGMNLRREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVPGDFANMLHLKELGLNNMEELVSIIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVHLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAEAGLYT
CVAQNLVGADETKTVSVVGRALLQPGRDEGQGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLILLAAGLA AHLGTQPRKGVGGRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGGGGACATTGTGACCGCCT
CTACATCGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCACCC
CCTGGCCACACTCTTCAAGATCCTGGCTCTTACATCAGCCTAGTCATCTTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCTCATGCTCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGCTTCTGTCGGAGGTGAGTGAAGAACAGCTGCGGAGCTGAACCTCAACAAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGCCTACCAAGAACCGCAGGACAAGCTGGAGCTGCACCTGTCATGCTAGGGCAT
CCCTGACACTGTGTTGAGCTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCGCC
CAGCATTGCCCAGCTCACGGGCTCAAGGAGCTGTCGGCTTACACACAGCGCCAAGATTGAAGCGCTGCGCT
GGCCTTCTGCGCGAGAACCTGCGGCGTGCACATCAAGTTACCGACATCAAGGAGATCCGCTGTTGATCTA
TAGCCTGAAGACACTGGAGGGAGCTGCACCTGACGGGCAACCTGAGCGGGAGAACACCGCTACATGTCATCGA
CGGGCTGCCGGAGCTCAAACGCTCAAGGTGCTGCCGCTCAAGAGCAACCTAACGCAAGCTGCCACAGGTGGTCAC
AGATGTGGCGTGCACCTGAGAAGCTGTCATCAACAAATGAGGGCACCAAGCTCATGTCCTCAACAGCCTCAA
GAAGATGGCGAACCTGACTGAGCTGGAGCTGATCCGCTGGACCTGGAGCGATCCCCACTCCATCTCAGCCT
CCACAACCTGAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATGAGGAGATCATAGCTCAGCACCT
GCACCGCCTCACCTGCCTAACGCTGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCG
CCTGGAGCGCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTCTTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAAACCTGACCTTCCCTGCCGACATCGGCCCTCTGAGAACCTCCAGAACCT
AGCCATCACGGCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGGCGAGCTGCGGGCCCTGACCT
GGGCAACAACGTGCTGCAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCG
CAACCGGCTGGAGTGCCTGCTGGAGCTGGCGAGTGCCACTGTCAGCGCAGGGCTGGTGGAGGA
GGACCTGTTAACACACACTGCCACCCGAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCTGAGCGAG
GCCGGCCCAGCACAGCAAGCAGCAGGACCGCTGCCGCTGGCAGGGAGCTGGAGCGCTGGGGCGCTTGTGAGTCAGGCCAGAGCGAGA
AACTCCGGACAGCCAGGACAGCCTCGCGCTGGCAGGGAGCTGGAGCGCTGGGGCGCTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGGCTGGCCCTTTCTCCCTCTGAGACTCACCGTCCCCCAGGGCAAGTGCTGTGGAGGA
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCCCTCCGGAGGGCAGCTGCTGCCAGGGCTGAG
CTGCCACCAGAGGTCTGGGACCCCTCACTTTAGTTCTTGTGATTATTCTCCATCTCCCACCTCCTCATCC
AGATAACTTATACATTCCAAGAAAGTTCAAGGGCCAGATGGAAGGTGTTAGGGAAAGGTGGCTGCCCTTTCCCC
TTCGCTTATTAGCGATGCCGCGGCCATTAAACACCCACCTGGACTTCAGCAGAGTGGCTGGGGCGAACCAAGCAGCCAGACAG
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGGCTCGGTGCGTCCACGGGAGAGCAGGCCCTCAGCTGG
AAGGCCAGGCCCTGGAGCTGCCTCTCAGTTTGTGGCAGTTAGTTAGTTTGTGTTTTTTTAATCAAA
AAACAATTTTTAAAGCTTGAAATGGATGGTTGGGTATTAAAAGAAAAAAACTTAAAAAA
AAAAGACACTAACGGCCAGTGAGTTGGAGTCTCAGGGCAGGGTGGCAGTTCCCTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCCCTTCCCTGGCGCAGGGTGCAGGGTGTCTCCGGATCTGGTGTGACCTGGTCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTGTGTTGGTTTTGGGTTTTGGTGTCTTGTGTTCTTCTCCTCC
ATGTGTCTGGCAGGCACTCATTCCTGTCGGCTGCGGCCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAAACGGTGCCTCCATTGCACTCCCTCTCGTGCCTGCCCTGCCCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTCGCCAGACTTGTGTTCCCCACCTCTGCGGCATGGGTGT
CCAGTGCCACCGCTGCCCTCGCTGCTTCCATCACGCCCTGTCGCCACCTGGTCTTCATGAAGAGCAGACACTTA
GAGGCTGGTCGGGAATGGGGAGGTGCGCCCTGGGAGGGCAGGCAGGCGTTGGTCCAAGGCCGTTCCCTGGCG
CTGGAGTGCACACAGCCAGTCGGCACCTGGGGCTGGAGGCAACCTGCTTAAAGTCACTCGGGTCCCCACCTT
AGAAGGGTCCCCGCCCTAGATCAATCAGTGGACACTAAGGCACGTTAGAGTCTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCAATTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGCAAAAATCCGTTACATGTGGGTCTGAACTTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFVDVDCVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQNLNNNEWTLRQRLTKNAQDKLELHLFMLSGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENRLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTLKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVQLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGCGCTCTCCGT
CCCGCGGTGGTTGCTGCTGCCGTGCTGGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACCTCTCAGAACTGCCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCGTGGCACTGGGTTCAAGTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGGTTCTCCTGAAGACCTCTTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGCGGGGGT
TGCCTTGGGTGATTCCCTGGATCTCCCTGTTGATTGGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTGTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACAGAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGTAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACATGGTCAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAECTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGCTGTGATCAAGAAGGTTCTGACCAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLKWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCCGCGCCTTATCAGGACCATGCGCCGA
CGGGTCATCACGTGCGCATCGTGGTGGAGAGGACGCCGACTCGGCTGGCGTGGCA
GGGGAGCCTGCGCTGTGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGG
CACTCACGGCGGCGACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGCTGCACCTGTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAAGGTGCCATCATAAACA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGGGAGGATGCCCTGCTCGGTGACTCAGGTGGACCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCAACTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCCAGGCCAGACCCCTCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTGTCTTGTAATTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLALLLARAGLRKPESQEAAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW
DSHVCGVSSLSHRWALTAAHCFETYSDSLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACACGCGTCCGGACCGTGGGAAGGGCAGA**ATGGACTCCAAGCCTGCTCCTAGGGCT**
CTTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTGGCGTGCAGGACCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAATGTGGAAAAGACTCTCGGAGCTGGTGCAGGCTGTGCGGATCCCAG
CTCTCCTCAATACGAAAATACCTGACCCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCCACACGGTGCAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGAAACCCATGTTGAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCCTGTGATCCGTAAGCGATAACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTCATGCCCTCTCGGTGGCAACTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTCCAACATCTCACCTGGGTCTACAGTAGCCCTGCCGGCATGAG
GGACAGGAGCCCTCCTGCACTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCTACATCCAGCAGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCCCTGCTCTGCCCTCAGGTGACAGT
GGGGCCGGGTGGTCTGTCTGGAAAGACACCAGTCCGCCCTACCTCCCTGCCCTCAG
CCCCATGTCAACCACAGTGGGAGGCACATCCTCCAGGAACCTTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCATG
CAGTGGCCGTGCCTACCCAGATGTGGCTGCACCTTCTGATGGCTACTGGTGGTCAGCAACA
GAGTGCCATTCCATGGGTGTCGGAACCTCGGCCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTGATGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCTGTAACAGGC
TGGGAACACCAACTTCCAGCTTG**TAAGACTCTACTCAACCCCTGACCCCTTCATC**
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCCCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTTTGAAATGCCCTCTCCCTCCGC
ATCTCATTTCTCTTCAATCAGGCTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCAATTCACTGCAAGGAGACCTCTACTGTCACTGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCCAGTGCATACTTCTCAATCTTGTGTTATG
GCCTTCCATCATAGTGCCCACCTCCCTCCTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGCTTCTCATCAATTCTGCTTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA
TCCATTGAGATTTGCTTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA
TCTACAACCAATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATAACCTCAA
TGTAaaaaaa

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTL ENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFH HYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVSGTSNNSQACAFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLM SAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLLFASGDGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILS LINEHRLSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHE SCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCCGGGCCACACCTGTCTGAGCGGCGCAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTTCCTTCTC
TTCTTCTGCTCTGTGCTGGCAAGTGAGCCCTAACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGTCGTCTGCCCAAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCCCTGGTGGCAGAGAACGATGTCCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTTCACTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCCTACAGCAATGCGATGCCAGCCAGGGCCAGGGCTGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGAGCGAAAAATTATTGGCATTTCAGG
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAGATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTCCTGGCAGCAATTAGGGCTTCTATGTTCTTATTAGGAGAGGCC
AAATTGTTTTGTCTGGCGTGACACGTGTGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAACTG
GTTTGTGTATCATATCATATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATTGACAATTAGTTAAAGTTAATCTCACGTTTG
CAAACTTGATTTCATCTGAACCTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLQPSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLYEEAKQYLSYETLYANGRTETQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVL
TAACIHDGKTYVKG
TQKLRVGFLKPKFKDGGRGANDSTS
SAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV
KDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIIGIFSGHQVDMNGSPQDFN
AVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGTCTCTGAGCCTGCTGCCCTGCTCCCCCGCCCCACCAGCCATGGTGGTT
CTGGAGGCCCTAGCCCTGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACGGGTTGGCGGCAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACAGCCGTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCCTGGTGGAGC
CCCACCTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCAGGCTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTG
CCCACCTCAGACCCCTGCAGAAGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGCGAGGGCTGTGCCGAGCGAACAGGCC
GGGTCTACATCAGCCTCTCTGCGCACCGCTCTGGTGGAGAAGATCGTCAAGGGTGCA
GCTCCCGGGCGCCTCAGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCG
CCGCGCCTCCTAGGCGCAGCGGACGCGGGCTCGGATCTGAAAGGCGGCAGATCCACA
TCTGGATCTGGATCTGCGCGGCCTCGGGCGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCTCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGGCCCCAGCGCTTTGTATATAATGTTAATGATTATT
AGGTATTGTAACCCTGCCACATATCTTATTATTCTCCAATTCAATAATTATTATT
CTCCAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFSTLLLASTAILNAARIPVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLFVLLGAWQLGNPGSRSQKVGVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGCCACCAATGCACGGCTCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCACCACAGGCCCGTGGAGGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGCCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGGGGCAC
AACAAAGGAGCGCGGGCGCCGCGAGAACTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCAAGACAGAGAGGATC
GGCTGTGGTCCCACTTCTGTGAGAAGCTCCAGGGTGGTGAAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCCTCCAAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAAC TGAGGCCCATCCTTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTGCGTAAC
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTTGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCCATCCCCAAATCAGCAGACAAAGTACAGACAAAAACA
AAAGTCCCTCTAGGAGCCAGAGAACTCTCTGGACCCAAAGATGTCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGCTTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCATGTGTGGGCCCTCTGGGA
CTACTGCTCTGCCTCTGGTGGCTGGAAATCTCTTGAATGGGATACCACCAAAGGG
TGAAGAGGTCACTGCTCTGTGTCATCTCCCCACCCCTGCCCCAGGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCCTCATCACACCCTC
ATCCTGGAGGCACAAGGCCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTGCCCTCCCTGGCTGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTTC
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPPLLLL VATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDMLHMRWDEE
LAAFAKAYARQC VVWGHNKERRRGENLFAITDEGM DVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAHS LPSLDEEPVTFPKS
THVPIPKSADKVTDKTVPSRSPENS LDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVV
SGLNSGPGHVGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTAGCTAGGCTTCAATTGGGAAGCCCCCTCAACAGAACCGTCAATTCTCCAAGTTATGGTGGACGT
ACCTCTGTTCTCCCTCTGCTTGCCTTACATTAGCAGACCGACTAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAGTCTCGCAAATATTACACTCTCTCCTGGCTGAAACAGGATTGTTGAAATACCTCCCTGA
ACATCTGAAAGAGTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGGTATTGACAA
TTTGGCCAACACACTCCTGTGTTAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTCGAATTGAACCGAAACAAGATTTAGATGGACTGACATTCCAAGGCCCTGG
TGCTCTGAAAGTCTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTGCAAGCTGAGCTGACCATAACAACTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGATGCT
GCAGGAACCTTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGCTTGCCAGAACGCTCAG
TGAGCTGGACCTAACTTCAATCAACTTATCAAGGTTAGATGATTCAAGGCTTCTGGCTAAGCTTACTAAATAC
ACTGCACATTGGAAACACAGACTGAGCTCATATTGCTGATGTCCTCCGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAACATGAAATTCCTGGACTATTGAAGACATGAATGGTGTCTTCTGGGTTGACAAACTGAG
GCGACTGTAACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGAACAGCAATCATGTCCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAATT
GCATTAAATACATCAAGCCTTTGCGATTGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACATT
TCAGAGCTTGTAATGCCAGTTGCTGCCCCATCTCAGCTGCTAAAGGAAGAACGATTTGCTGTTAGCCAGA
TGGCTTGTGTGATGATTCCAAACCCCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGTCAGCTGCCAGCAGCAGTGATCCCCATGACTTTGCTTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGAAAATTATGCACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACCAC
CATCCCTGGCTGCGAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTATCTCCAATCACTTTGGTTC
ATCCTACTCTGTCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCCT
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGTGGGACCCAGCCCCCAGATAGCCTGGCAGAACGGA
TGGGGGACAGACTTCCAGCTGCACGGGAGAGACGCATGATGTGATGCCAGGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAGCAAATGC
AACTCTGACTGTCCTAGAACACCATCATTTTGGGCCACTGTTGGACCGAACGTAAACCAAGGGGAGAAACAGC
CGTCTACAGTCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAGATGATAGCCCATTGGGGT
AACCGAGAGGCACTTTTGCAAGCAGGCAATCAGCTCTGATTATTGGAACATGAGTGTGATGCTGGGAA
ATACACATGTGAGATGCTAACACCCCTGGACTGAGAGGAAACGTGGCCCTAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCATGAGACAGCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTCATAGC
CGTGGTTGCTGTGGGGCACGTCCTCGTGTGGGTGTCATCATATACCAACAAGGGGAGGAATGAAGA
TTGCAGCATTACCAACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTCATCTCAGGGAACGTT
AGCTGACAGGCAGGATGGTACGTGCTTCAGAAAGTGGAGGCCACCCAGTTGTCACATCTCAGGTGCTGG
ATTTTCTTACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGC
CACAGATCTGTTCTTGTCCGTTTGGGATCCACAGGCCCTATGTTGAAAGGGAAATGTGATGGCTCAGA
TCCCTTGAAACATATCATACAGGTTGCAGTCTGACCCAGAACAGTTTATGGACCAACTATGAGGCCAGTT
CATAAAGAAAAGGAGTGTCTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTCAGTAATATATC
GTGGCTTCACATGTGAGGAAGCTAACACTAGTTACTCTCACAAATGAAGGACCTGGATGAAAATCTGTG
TCTAAACAAGTCTCTTAAAGTGTGAAATCCAGAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCTGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACAGCCATCAGATTGTCAGCC
AAGAGCCTTTATTGAAAGCTATTCTCCAGACTTGGACTCTGGTCAGAGGAAGATGGGAAAGAAAGGAC
AGATTTCAGGAAGAAAATCACATTGACCTTAAACAGACTTTAGAAAACACTACAGGACTCCAAATTTCAAGTC
TTATGACTTGGACACATAGACTGAATGAGACCAAGGAAAAGCTTAAACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAAATCTTATGTTAAATGGAGTTATGAATTAAAAGGATAAAAATGCTTATTATACAGAT
GAACCAAATACAAAAGTTATGAAAATTCTTATGTTACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA
TTTTTAACTTTGTTTATGCAAAAAGTATCTACGTAATTAAATGATATAAAATCATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGTACCAATT
TTAAATAGAAGTTACTTCATTATATTGACATTATTTAAATAAAATGTGTCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSIKASSMSHLQLSREVKLNNNELETIPNLGPVSANITLLSLAGRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGYFDNLANTLLVLKLNRRNRI SAI PPKMFKLPQLQHLELNRRN KIKNVDGLTFQGLGALKSLKMQRNGVTKLMDGAFWGLSNMEI LQLDHNNLTEITKGWLYG LMLQELHLSQNAINRIS PDAWEFCQKLSELDLTFNHLSSLRDDSSFLGLSLLNLT HIGNRVSYIADCAF RGLSSLKTL DLKNNEISWTIEDMNGAFSGLDKLRRRLI LQGNRIRSITKKAFTGLDALEHLDLSDNAIMS LQGNAFSQMKKLQQLHLNTSSLLCDCQLKWL PQWVAENN FQSFVNASC AHPQLLKGRSIFAVSPDGFVCDDFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGEVMEYTTI LRLREVEFASEGKYQCVISNHFGSSY SVKAKLTVNMLPSFTKTPMDLTIRAGAMARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVY SCTAQNSAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPP KLNWTKDDSP LDDG WATVGVIIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNLPADIPSYLSSQGT LADRQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGP MYLKGNVYGS DP FETYHTGCSPD PRTVLM DHYEPSYIKKKEC YPC SHP SE E CERSFSNISW PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLDF SANPEPASVASSNSFMGTFGKALRRPHLDA YSSFGQPSDCQ PRAFYLK AHSSPDLD SGSEEDG KERTDFQEE NHICTFKQTLE NY RTPNFQS YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459, 628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268, 314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653, 671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962, 1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534, 612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGAAAAGGAGACTTTTTGGTGGTGGCTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAAGAGTTAGACCCGCGGGGTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAACAAAGAAAAAGTATGTTCATTTC
TATAAAGGAGAAAGTGAGCAAGGAGATATTGGAATGAAAAGTTGGGGCTTTTTAGTAAAGTAAGAAC
GGTGTGGTGGTGTCTTCTTGTGAAATTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTGAACCCGGCAGATTGAGGCATTGATTGGGGAGAGAAACAGCAGAGCACAGTTGGA
TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCACTGGATTTCATCAACCTCCTTTTTTAAAT
TTTATTCCCTTGGTATCAAGATCATGCGTTCTCTGTTCTTAACACCACGGATTTCATCTGGATGTTGCT
GTGATCAGTCAAATACAATGTTGAATTCCAGAACAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGC
GCTGGCTCTTCAACTTCTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTCTGTGCTCTGAGCAA
CCAGTTCAAGGTGATTGTGTTGGAAAAACCTCGCTGAGGTTCCGGATGGCATCTCCACCAACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCATTGAGGCATTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGGAACCTCAACACTCTGGA
ACTTTGACAATCGTCTTACTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTGGTT
GCGAACACAACCCATTGAAAGCATCCCTTATGCTTTAACAGAAATTCTTCTTGCGCCACTAGACTTAGG
GGAATGAAAAGACTTTCATACATCTCAGAAGGTGCCCTTGAGGCTGTCCAACCTGAGGTTATTGAAACCTTGC
CATGTGCAACCTCGGAAATCCCTAACCTCACACCGCTCATAAAACAGATGAGCTGGATTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTCCAGAT
TCAAGTGAACGGAAATGCCCTTGACAACCTCAGTCAGTGGAGATCAACCTGGCACACAATACTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGACATCTAGAGCGGATACATTACATCACACCCCTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCTCGAACACAGCTTGTGCCCCGGTG
TAACACTCCCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCGAGATTACTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGCAGCTGAGCTGAAATGTGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAATGGAACACTCATGACACATGGGGCTACAAAGTGGGATAGCTGT
GCTCAGTGTGATGGTACGTTAAATTTCACAAATGTAACCTGTGCAAGATAACAGGCTATGACATGTTGAGTAA
TTCCGGTGGGAATACTACTGTCTCAGCCACCTGTAAGTACTGTGAGGACTACTCCTTCTTACTTCC
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACACAGATAACAAATGTGGTCCCAC
AGTGGTCAGTGGAGACCACCAATGTGACCACCTCTCACACCAAGAGCACAGGTCGACAGAGAAAACCTT
CACCACCCAGTGAATGATATAAACAGTGGGATCCCGAGGAATTGATGAGGTCATGAAGACTACAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGAGTGTGCTGGTATTTCACAAAGATGAGGAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAGGACTGTGAAATTATTAAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCGTATGAGCATGAGCACCTAAACTATAACTCACAAATCTCCCTT
CAACCAACACAACAGTTAACACAATAATTCAATACACAGTTGAGGCTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAACAAACAATCAAAAAAAA
GACAGTTATTAAAGACACAAATGACTGGCTAAATCTACTGTTCAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTAAAGTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYILNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLPHDLFTPPLHHLERIHLHHNPWCNCIDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNSVGN
TTASATLNVTAAATTTPFSYFSTVTETMEPSQDEARTTDNNVGPTVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAILMAAVMLVIFYKMRKQHHRQH
HHAPTRTVEIIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGCAGTTCTTTCGGTTCCCTCCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCGAGGGAGGAGCGCGCACCGCACCG
GAGGGCGGGCGTGCACCCCTCGGCTGGAAGTGGTGCCTGGGCCCCGAGCGCGCGCGCGGGCTGGAGCTTCGGGTAGA
GACCTAGGCCGCTGGACCCGATGAGCGCCGAGCCTCGTGCAGCGCCGCGGGTTGGGCTGCTGCTGTGC
GCGGTGCTGGGCCGCTGGCGTCCGACAGCGGGTGCCTGGGGACTCGGGCAGGCCCTCTGGGTAGCCGCC
GAGGCCCATGCCCTCGGGTGCCTGGACTTAAGTCACAAAGATATTCTTCATCAAGGCAAGTCC
CCCGAGCCACTCCGCTCTGGTGCCTGGACTTAAGTCACAAAGATATTCTTCATCAAGGCAAGTCC
ATGAGGCCACTTCAAAGCCTTCAGAGAAGTGAAGACTGAACACAATGAATTGGAGACCATTCAAATCTGGGACCA
GTCTGGCAAATATTACACTCTCTCTGGCTGAAACAGGATTGTTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCTTGAAACTTTGGACCTTAGCAGCAACAATATTTCAGAGCTCAAACGTCATTCCAGCCCTACAG
CTCAAATATCTGTATCTAACAGCAACCGAGTCACATCAATGAACTGGTATTGGACAATTGGCAACACA
CTCCTGTGTTAAAGCTGAACAGGAACGAATCTAGCTATCCCACCAAGATGTTAAACTGCCCAACTGCAA
CATCTGAATTGAACCGAAACAAGATTAAAATGTAGATGGACTGACATTCAAGGCCCTGGTGTGCTGAAGTCT
CTGAAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGAAATTGG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGTGATGCTGCAGGAACCTCAT
CTCAGCCAAATGCCATAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAGCTCAGTGAGCTGGACCTA
ACTTCAATCACTTACAGGTTAGATGATTCAAGCTTCTGGCTAACGTTACTAAATACACTGCCACATTGGG
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAGAAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGCTGACAAACTGAGGGCAGTGTACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTTCACTGGTTGGATGCACTGGAGCATCTAGACCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCAATTCAAATGAAGAAACTGCAACAAATTGCAATTAAATACA
TCAAGCCTTGTGCGATTGCCAGCTAAATGGCTCCCACAGTGGTGGCGAAAACAACACTTCAAGAGCTTGT
AATGCCAGTTGTGCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGTCTGTTAGCCAGATGGCTTGTGT
GATGATTTCCTAAACCCCAGATCACGGTTGCCAGAAACACAGTCGGCAATAAAAGGTTCAATTGGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTTGGAAAAAGACAATGAACACTACTGCATGAT
GCTGAAATGAAAATTATGCAACACCTCCGGGGCCAAGGGTGGCAGGATGGAGTATACCAACATCCTCGCTG
CGCGAGGTGAAATTGCGCAGTGAGGGAAATATCAGTGTGCTATCCTAACAGACCCCCATGGATCTCACCGAGCTGGGCC
AAAGCCAAGCTTACAGTAAATATGCTTCCCTATTCAACAGACCCCCATGGATCTCACCGAGCTGGCAGAAGGATGGGCCAGAC
ATGGCACGCTGGAGTGTGCTGTGGGCCACCCAGCCCCCAGATAGCCTGGCAGAAGGATGGGCCAGAC
TTCCAGCTGCACGGAGAGACGCACTGATGTGATGCCAGGATGACGTGTTCTTATGTGGATGTAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTCAAGCAACTCTGACTGTC
CTAGAAACACCATCATTGGCGCCACTGTTGGACCGAACCTGTAACCAAGGGAGAACAGCCGCTCACAGTGC
ATTGCTGGAGGAAGGCCCTCCCCCTAAACTGAACCTGGACCAAGATGATAGCCCATTGGGTTAACCGAGAGGCAC
TTTTTGAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGCTGGAAATACACATGTGAG
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGTGATCCCACCCAACCTGCACTCCCT
CAGATGACAGCCCCATCGTTAGACGATGACGGATGGCCACTGTGGGTGTCGTGATCATAGCCGTGGTTGCTGT
GTGGGGCACGTCACTCGTGTGGTGTGATCATATACCACACAAGCGGAGGAATGAAGATTGCAACATTAC
AACACAGATGAGACCAACTGCCAGCAGATATTCTAGTTATTGTGATCTCAGGAAACGTTAGCTGACAGGCAG
GATGGGTACGTTCTCAGAAAGTGGAGGCCACCACTGTCACATCTCAGGTGCTGGATTCTTACCA
CAACATGACAGTAGGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGTGAGCTGCCACAGATCTGTT
CTTGTCCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGATCTTGTGAAACA
TATCATACAGGTTGCACTCTGACCCAAAGAACAGTTTAATGGACCACTATGAGCCAGTTACATAAAGAAAAG
GAGTGTACCCATGTTCTCAGAAGAACTCTGCCAACGGAGCTTCAGTAATATATCGTGGCTTAC
GTGAGGAAGCTACTTAACACTAGTTACTCTCACAATGAAGGACCTGGAAATGAAAATCTGTGCTAAACAAGTCC
TCTTGTGTTTAAATGGAGTTATGAAATTAAAAGGATAAAATGCTTTATTTATACAGATGAACCAAATTAC
AAAAGTTATGAAAATTTTATACGGGAATGATGCTCATATAAGAAATACCTTTAAACTATTTTTAACTT
TTTATGCAAAAAGTATCTACGTAATTAAATGATAATCATGATTATTTATGATTGTTATAATGCCAGA
TTCTTTTATGGAAATGAGTTACTAAAGCATTAAATAACCTGCCTGTACCATTTTAAATAGAAGTT
ACTCATTATATTGACATTATTTAATAAAATGTGCAATTGAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASAPPKMFKLQPQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAIRISPDAWEFC
QKLSLELDLTFNHLRSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDLKNNEIS
WTIEDMNGAFSGLDKLRRLLILQGNRIRSITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCACHPQLLKGRSIFA VSPDGFCDDF
PKPKQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRVTKGTAVLQCIAGGSPPPKNWTKDDSPLVVTERHF
FAAGNQLLIVDSDVSDAGKYTCEMSNTLGERGNVRLS VIPTPTCDSPQMTAPS LDDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRNEDCSITNTDETNL PADIPS YLSSQGT LADRO
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDFETYHTGCPDPRTVLMHDYEP SYIKKKECYPCHPSEES CERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLKAHSSPDLSGSEEDGKERTDFQEEHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGAGAGCGCCAGCTTGAATGGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGAGCGCGTTCGGCCTGTGGGCGCCGCTGGCGCCGGCGCAGCAGGGAAAGGGAAAGCTGTGGCTGCC
CTGCTCCACGAGCGCCACTGGTGTGAACCGGGAGAGGCCCTGGTGGTCCCCTATCCCTCCTTATATA
GAAACCTCCACACTGGGAAGGCAGCGCGAGGAGGAGGCTATGGTGAAGCAAGGAGGCCGGCTGATCTGCAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCGAGGAGGAGAACAGCCTGCCCTGGT
TCCATCAGCCCTGGCGCCAGCGCATCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGGCCGGGTGCTGC
TGCTCTGCTGCTGCTGCCACAGCTGCACCTGGACCTGTGCTTGCCTGAGGGCCAGGAGGATTTGGCCGAA
GTGGCGGCCACAGCCTGAGGCCGAAGAGAACGAATTGCGGAGGAGGAGGCCGGTGTACTGAGCCCTGAGG
AGCCCGGGCTGCCCCAGCGCGTCACTGCCCGAGACTGTGCCTGTTCCAGGAGGGCTCGTGGACTGTG
GCGGATTGACCTGCGTGAGTCCCGGGGACCTGCCCTGAGCACACCAACACACATCTCTGCAGAACAAACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCGGCTGCACCGGCTGGAGACACTGAACACTGCAAACAAACCGCTGA
CTTCCCGAGGGCTCCAGAGAACGGCTTGAGCATCTGACCAACCTCAATTACCTGACTTGGCCAATAACAAGC
TGACCTTGGCACCCCGCTTCTGCAAACGGCTGTGATCAGTGTGGACTTGTCTGCCAACTATCTCACCAAGATCT
ATGGGCTCACCTTGGCAGAACGCAAACCTGAGGTCTGTGTACCTGCACAACAACAGCTGGCAGACGCCGGC
TGCCGACAACATGTTCAACGGCTCCAGCAACGTGAGGTCTCATCTGTCCAGCAACTTCTGCGCACGTGC
CCAAGCACCTGCGCCTGCCCTGTACAAGCTGCAACCTCAAGAACAAAGCTGGAGAAGATCCCCCGGGGCT
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCCAGCCTGGAGTACCTGGATCTGTCCAGCAACAACCTGTCTCGGGTCCCAGCTGGCTGC
CGCGCAGCCTGGTGCTGCTGCACTTGAGAAGAACGCCATCCGGAGCGTGGACGCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCAAGCAACCAAGCTGCGGGAGCAGGGCATCCACCCACTGGCCTTCAAGGGCC
TCAAGCGGTTGACACGGTGCACCTGTACAACAACCGCCTGGAGCGCTGCCAGTGGCCTGCCCTGCGCGTGC
GCACCCCTCATGATCTGCACAACCGAGTCACAGGCAATTGGCGCGAAGACTTTGCCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCACAGGTGACCGCGACGCCCTCGCAAGCTGCGCCTGCTGC
GCTCGCTGGACCTGTGGCAACCGGCTGCACACGCTGCCACCTGGCTGCCTGAAATGTCCATGTGCTGAGG
TCAAGCGCAATGAGCTGGCTGCCCTGGCACAGGAGGGCGCTGGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGGCCCTGGCCCCCGTGCCTGGTGGACCTGCCCATCTGAGCTGCTGGACA
TCGCCGGGAATCAGCTCACAGAGATCCCGAGGGCTCCCGAGTCACCTGGAGTACCTGAGCTGCTACCTGCAGAACACA
AGATTAGTGCCTGGCCGCAATGCCCTCGACTCACGCCAACCTCAAGGGGATCTTCTCAGGTTAACAAAGC
TGGCTGTGGCTCCGTGGTGAGCTGCTTCCGGAGGCTGAAGCACCTGCAGGTCTGGACATTGAAGGCAACT
TAGAGTTGGTGAACATTCAAGGACCGTGGCCCTTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAGGTGATGAGATGTGACCTAGGATGATGGACCGCCGGACTCTTTCTGC
AGCACACGGCTGTGCTGAGCCCCCACTCTGCCGTGTCACACAGCTCATATCCCCACCCCTCCACGGCGTCCACGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCACACACAACCTACCCCTCAAACCCACACAGTCTCTGTCACAC
CCCCACTACCGCTGCCACGCCCTGTGAATCATGAGGGAAAGGGCTGCCCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGTATGCGTATGCATACACACCACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCAAAGCCTATGCCACAGACAGCTTGGCCAGCCAGAATCAGCCATAGCAGCTGCCGTGCCCT
GTCCATCTGTCCTGCCGTTCCCTGGAGAAGACACAAGGTATCCATGCTCTGTGGCCAGGTGCCACCCCT
GGAACTCACAAAGCTGGTTTATTCTTCCATCCATGGGACAGGAGCCTCAGGACTGCTGGCCTGGC
TGGCCACCCCTGCTCCAGGTGCTGGCAGTCACTCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCAGTTTCAATGGGAAGGCCAGTGGAGGCAGGATGGAGAGGCCCTGGTGCTGCTGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGAGGAAGGACCCAGCTGCACCTAGGAGAACCTT
GTTCTCAGGCCGTGGGGAGTCCGGGTGCCATTATTCTTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTGTTATAGAAAAACTAATATAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENFAEEEVLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLQLQNNQLEKIYPEELSRLHRIETLNLQNNRLTSRGLPEKAFLTNLYLYLANNK
LTLPAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVAGLPRSLVLLHLEKNAIRSVDANVTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRTLMILHNQITGIGREDFATTYF
LEELNLSSYNRITSQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCCCTGCCCTCGCCCTGCTCCCTCCGGAGGGCAG
CACTAGCCCGGGCGCGAGGGCTGGGGGTTCTCGAGACTCTCAGAGGGCGCTCCCATCGCGCCACCCACCC
CAACCTGTTCTCGCGCGCACTGCGCTCGGCCAGGACCCGCTGCCAACATGGATTTCTCCCTGGCGCTGGT
GCTGGTATCCTCGCTCACCTGAGGGCGCGAGGTTGACAGGGAGGTGGCCAGGAAATAGTGTATCGAT
TGGCTATGCTGTTATGGTGGAGGATTGACTGCTGCTGGGCTGGCCAGTCTGGGAGCTGGTACAGTGTACGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGCCAACACAAGTGAAGTGTATCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGGGCCCTGTAAGCACAGGTGCATGAACACTTA
CGGCAGCTACAAGTGTACTGCTCAACGGATATATGCTCATGCCGATGGTCTGCTCAAGTGCCTGACCTG
CTCCATGGCAAACATGTCAGTATGGCTGTGATGTTGTTAAAGGACAAATACGGTGCCAGTGCCTGCCATCCCCCTGGCCT
GCACCTGGCTCTGATGGGAGGACCTGTGAGATGTTGATGAATGTGCTACAGGAAGAGCCTGCCCTAGATT
TAGGCAATGTGTCACACTTTGGAGCTACATGCAAGTGTCACTGGTCAGTATCAGTGCAGCAGCTTGCTGATGTTAA
CAAATATCAATGTCATGACATAGACGAATGCTCACTGGTCAGTATCAGTGCAGCAGCTTGCTGATGTTAA
CGTACGTGGGCTCTACAAGTCAAATGAAAGGATACCAAGGGTGTGACTGACTTGTGTTATATCCAAA
AGTTATGATTGAAACCTTCAGGTCAAATTGATGACCAAAGGGAAATGGTACCATTTAAAGGGTGACACAGGAAA
TAATAATTGGATTCTGATGTTGAAAGTACTTGGTGGCTCCGAAGACACCATATATTCTCTCTATCATTACCA
CAGGCCTACTCTAAGCCAACAACAGACCTACACCAAGCCAACACCAATTCTACTCCACCAACACCAC
CCTGCCAACAGAGCTCAGAACACCTTACACCTACAACCCAGAAAGGCCAACACCGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACGCCCTCAGAAACCCAGGAG
AGATGTGTTCTGGTACACAGTTGATGTTAAAGGACTGGGATTGGATGGATCAGGGAGAAAGACAA
TGACTTGCCTGGGAAACCATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAGGCCAGG
GGGAAAAGCTGCACGCTGGTGTACCTCTCGGCCCTCATGCATTAGGGGACCTGTGCTGCTGATTCAAGGCA
CAAGGTGACGGGCTGCACTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCCTGCCAGGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCATGGCTGGAGGCAAACACAGATCACCTTGCAGGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAAGATCTATGATGAAATTTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
AGAAGACTGAGGGGCAAACCATGGTGGTTCAAGTATGAAAGGGTTGGCACAGAGAGGGTGGCAGCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGATGATAAGGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTTCATAAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAAATTAGA
AAAAAATTGTCATTAAAGATGGTAAAGATGTTCTACCAAGGAAAGTAACAAATTATAGAATTTCACCAAA
AGATTTTGATCTACTAGTAGTATGCACTGGTGGTTCAAGTAAAGGAAACTTCTAGAATTTGACAAAGGCTTAATTAGG
CATTCCTCTGACCTCTAATGGAGAGGGATTGAAAGGGGAAGAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATCTCAGTATTAAAGAAAAAGGAAACTATTATCCAAATGAGAGTATGATGGAC
AGATAATTAGTATCTCAGTAAATGCTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTCAAGATTTTTTTAAGAGATCCTCAAGGAACACAGTTAGAGAG
ATTTTCATGGGTGCATTCTCTGCTCGTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC
ACACCGCAGACCTTCTCACCTCATCAGTATGATTCAAGTCTCTTATCAATTGGACTCTCCAGGTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAACGGTCTCTGTCAATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTAAATGTTCAATGGTTCATT
TCCTTATGGTCATAACTGCACAGTGAAGATGAAAGGGAAAATAATGAAATTTACTTTGATGCCAA
TGATACATTGCACTAAACTGATGAAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCCAATGGCTAATAAAAACAATTATGAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGC DVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTT PERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVF SVL VHS CNFDHGLCGWI REKDNDLHWEPI RD PAGGQYLT VSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTAAGGTCTCACAACTTCCCTTGCAACAGGTGCTGCTGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATGGCTATTGAGAGACCCA
ACAATGCCAAATACTACTGGGCTGTGAATAAGTCTGGTCTGACTTGAATACC
AACACAAGTTCACCATGATGCCACCCAATGCATCTGCTTATCAACCCACTGCAGTCCCT
GATGAAGGCAATTACATCGTAAGGTCAACATTCAAGGAAATGGAACTCTATGCCAGTCA
GAAGATAACAAGTCACGGGTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTCATCCTCCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCACCCTACTCCTTT
TCCCCAAAACAATACCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGAATTACAGCT
GCCTGGTGAGGAACCTGTCAGTGAATGGAAAGTGTATATCATTATGCCCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAGCATGGCCTCGTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTACAGTTACACTCCGTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATGTACCTTAGCAAGTATAACTGGAATATCACTATTTTGATT
ATATCCATGTGCTTCTCTTCTATGGAAAAAATATCAACCCCTACAAAGTTATAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAAATACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAAATATATGAATTGTTGCTTTCCAGATGTTCTGGTGTTCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGCAAGATTGACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCACCCAGAGTGAACATTGATGG
GCTAAACAGTACATTGAGTGAAAATTCTGAAGAAACATTAAAGGAAAACAGTGGAAAAGT
ATATTAATCTGAATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATCCTTACA
TGCAGAATAGAGGCATTATGCAAATTGAACCTGCAGGTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGAAATATTCCCTAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGTTCTCATAGTTGTATGAAATATCTACAAACCTCA
ATTAGTTCTACTCTACATTCAACTATCATCACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTACATTGTTGCAATTATTCAGCAGACTTGTGTTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCAGCAGACTTGTGTTATTGACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAAACATGCCCTCTCTTTTTCAATCACC
AGTAGTATTGAGAAGACTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTGCTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNSDKGLKVGEVFTV
DLGEAILFDCTSADSHPPNTYSWIRRTDNTTYIIKGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGCGAAATGGCGCCCTCCGGGAGTCTCAGTCCCTGGCAGTCCTGGTGTGTT
GCTTGGGGTGTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT
TGTCAAAAATCTTCAACCGGAATGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTTATAAGTGTATAAGAGTGGAAAGAGTATTGAGGCCTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGGGATGAAGAA
GATGTTCAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAGACAACGCTCTGGTCCATCATTGCCACAGATAAATCCTAGTTAATTTATAG
TTATCTTAATATTATGATTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAAGGTTCAGTCTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTTACAAAGTTGAAATTGATTTAAGCACAGTTATGATG
GTTAAATAGTTCTCTATTTGAAAAATCGTGCCAAGCAATAAGATTTATGTATTTGT
TTAATAATAACCTATTCAAGTCTGAGTTTGAAAATTTACATTCCCAAGTATTGCATT
TGAGGTATTTAAGAAGATTTTTAGAGAAAAATTTCTCATTTGATATAATTTTCTCTG
TTCACTGTGAAAAAAAGAAGATATTCCATAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGTATTCAGTGACAAATTCGTGGCTTTTAGAGGTTATTCCAAATTTCTTGT
ATTTTTAGGTTTATGCAACTAAAAACTACCTTACATTAATTACAGTTCTACAACA
TGGTAATACAGGATTGCTACTGTGATTAGGAAGTTTAAGTTCATGGTATTCTCTGATTTC
CAACAAAGTTGATTCTCTGTATTTTCTTACTACTATGGGTTACATTTTATTTTT
CAAATTGGATGATAATTCTTGAAACATTTTTTATGTTTTAGTAAACAGTATTTTTTGTT
GTTTCAAACTGAAGTTACTGAGAGATCCCATCAAATTGAACATCTGTTGTAATTTTAAATT
TTGGCCACTTTTTCAGATTTTACATCATTCTGCTGAACTTCAACTGAAATTGTTTTTT
TTCTTTGGATGTGAAAGGTGAACATCCGTATTTTGTCTGATGTAAAAGCCTGGTA
TTTTACATTTTGAAAAATTCAAGAAGCTTAATATAAAAGTTGCCTCATATACAAGAAAGTTCTAAATTG
TTACAGTCTGTAAGTGTTAAAATATAACATTTTTATTTTTAAAGACAA
ACTTCATATTATCTGTGTTTCTCTGACTGGTAATATTGGTGGGATTTCACAGGTAAA
GTCAGTAGGATGGAAACATTTAGGTATTTTTACTCCTTAAAGAGCTAGAATACATAGTT
CACCTTAAAGAAGGGGGAAATCATAAATACAATGAATCAACTGACCATTACGTAGAC
AATTCTGTAAGTGCCCTTCTTTGCTGCTGGTGAATCCATTAGATTTACAG
TATCGTAAATACAAGTTTCTTTAAAGCCCCTCCTTTAGAATTAAAATATTGTACCATT
AAAGAGTTGGATGTGTAACTGTGATGCCTTAGAAAAAATCTAAGCACAAAAAACCT
TTCTAACCACTTCATTAAAGCGTAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCCGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGGGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGCCCTGGTTGGTGTCTGAGCTGTGTCAGGCCAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGCCCTGCCGGAGGACCTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGCAAGGGCAGTTCTCCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGAACTTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCAACCGTGCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGGATCTGCCGTACTTGAGCAGTTATTGGA
GGAAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGGCTGTGGACTACCTGCTGAGAGGGATGTTACGAGAGCCTCTGCGTGGG
GAGGGTGTCAAACGTACACCCCGTAGACAGAAGAGGCTTCTGTAGGTACCAACATGGCA
CAGGGCCCCACAGCTGCTCATGCCCTTCAAAGAGGAGGACGAGTGGACAGCCCGACA
TCGTCAGGTACTACGATGTCATGCTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAA
CCTAAACTGCACGAGCCACCGTTGATCCAAGACAGGAGTCCTACTGCGCAGCTA
CCGGGTTTCCAAAAGCTCTGGTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC
GTCGGATGCGCATATCACAGGGTTAACAGTAAGACTGCGAGATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTCGACTTCTCTAGGCGACCTTGTACAGCGG
CCTAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC
TGTGCTTGTGGCTGCAAGTGGGTCTCCAATAAGGTTCCATGAACGAGGACAGGAGTCT
TGAGACCTGTGGATCAACAGAAGTTGACTGACATCCTTCTGCTCTCCCTCTGGTC
CTTCAGCCCATGTCACAGTACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCAGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTCCATTGCGCTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGAGCAGAGTTAGCTGCTAGCGCTAGCAAGGTGCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACCAAAAAATGTCCCTACCAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPAGEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQLVKQLDAGEEATTKSQVLDYLSAVFQLGDLHRALELTRRLLSLDPSPHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHGNRAPQLLIAPFKEEDEWDSPHIVRYDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYVGGQYEPHFDFS
RRPFDGLKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEGDYL
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCTTTAGTGGAAAGACAGACCATATAATCCAGTGTGAGTGAAATTGATTGT
TTCATTATTACCGTTTGGCTGGGGTTAGTCCGACACCTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTCTGGGATGCTGGTCTGGAAGCCAGCGGGCCTGCTCTGTCTTGGCCTCATGACCC
CAGGTTCTCTGGTAAAGCTACTACTGGCCTGGTCCCCTCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGGCACCCACCTGGCAGGGCTACCACCATATGCACTGAGCTCCCTGTTGGCTCTGCTGCGGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTGGGGTGCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCCCTACTACAGGGACCCCAACAAGCCCTACAAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGCTGTCTGACCTCCCGAGCTACACTGTCCA
CTTGGCCGTGGCTGTGAACCGTACGGTGGCCATCACTTCCCTCGTTACTCTACTTCACTGGGAGCGGGGG
CCCGGGCTCCAGCAGGGATGCAGGTGGTGTCTCATGGGATGAGCGGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGGCCACTACGACTGGTTCTCATCATGCAAGGATGACACATATGTGAGGCC
CCCGCCTGGCAGCCCTTGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCAATTG
GCGCAGCGAGCAGGCCGTTACTGTCTGGGGCTTGGTACCTGGTGTACGGAGTCTCCTGCTCGTCTGC
GGCCACATCTGGATGGCTGCCGAGGACATTCTCAGTGGCCCTGTACGAGTGGCTGGACGCTGCCCTATTG
ACTCTCTGGGCGTCGGCTGTCTCACAGCACCAGGGCAGCAGTATGCTCATTTGAACGGCCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGGCTTCGCGTGTGACCGCTGTCTCCGAAGGTACCCCTCATGT
ACCGGCTCCACAAACGCTTCAGCGCTTGAGTTGGAGCGGTTACAGTGAACATAGAACAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGCTGACCCCGAAGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCAACTCTCGTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTGAGATGGGG
CTCCCAAGTGCCCAACTACAGGGGCTAGCAGGGGAGCTGGTGTGAGCTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCCTATCAGCCCCGCTGCGCTTCCAGAACAGCAGCAGTGTCAACGGCTATGGCGCTTCGACCCAGCAC
GGGGCATGGAGTACACCGTGGACCTGCTGTTGGAAATGTGTGACACAGCGTGGCAGGGCCCTGGCTCGCA
GGGTAGCCTGCTGGCCACTGAGCCGGTGGAAATCCTACCTATGCCCTATGTCAGTGGCCACCCGAGTGC
AGCTGGTGTGCCACTCTGGTGTGAAGCTGCTGAGCAGCCGGTTCTCGAGGCCAATGTCC
TGGAGGCCAGAGAACATGCAATTGCTCACCTGTTGCTGGTCTACGGGCCAGGAGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGGTGAAGGCTGCAAGCAGCGGAGTTAGAGCAGGGTACCTGGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCACTCATGGACGTGGTCTCGAAGAACGACCCCTGTGGACACTCTCT
TCTTCCCTTACCAACCGTGTGGACAAGGCCCTGGGCCAGTGGCTCAACCGCTGTGCGATGAATGCCATCTGGCT
GGCAGGCCCTCTTCCAGTCCATTCCAGGAGTCAATCTGGCTGACCCCTGGCTCAGGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCCCCTCCCTGGTGTGACCCCTCCCGGGGGCTCTATAGGGGGAGATTG
ACCGGCAGGCCCTCTGGGGAGGGCTGCTTCTACACCGCTGACTACCTGGCGGCCAGCCGGCTGGAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTCTCCTGGCTCAGGGCTCC
ACCTCTTCTGGGGCTAGAGGCCAGGGCTGGTGCAGAAGTCTCCCTGGCTGAGACTGCAGCCCACGGCTCAGTGAAG
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGGCGTGCCCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCCTGGGGCCCTAACCTCATTACCTTGTCTGCCCTCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGACAGATAAGAGAATTGTTGCTGATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSQHDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDS LGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLLC VTQRGHRRALARRVSLLRPLS RVEILPMPYVTEATRVQLVLPPLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLRNCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEAELEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRAGQLAMALFEQEQANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACCGTGGAAACCGTGGCTGCCTTCTGTCCCCAAGCC
GTTCTAGACCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTGAAAATTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTCGAGTACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGGCTGCAGTAAAGGAGACTGGACCAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATATGGCTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTTGGCATTTCAT
GATGCATTGGTTCTTACCTCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGATAGGACGTGTGTCATTATTGTAGTAGTAACATACATCCAA
TACAGCTGTATGTTCTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTGGAAAGAAGTGTGTTAAGAATAATAATTTGCAAATAACTATTAAATAATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTGCTGATTGGTT
AAAAAATTAAACAGGTCTTAGCGTTCAAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACTTTAGCTGTGTGTTCCCTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACAGCAACTAAAGAAA
ATTAAAGTGAAGTGGAAAAAT

FIGURE 120

MLSSESSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSENVKFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTTCTTCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCCATCCTATTCTCAGTGCCTGTTCATCACCAGATGTGTTGTGACATTCGCAT
CTTCAAAACCTGTGATGAGAAAAAGTTCAGCTACCTGAGAATTCACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGTCCATTGAACGGAAATATTTCAATCC
AGCTGCTACTTCTTTCTACTGACACCATTCTGGCGTTAAGTTAAAGAACTGCTCAGC
CATGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCTTCTACAAGA
AACCTAAAATGAGAGAGTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGCCAAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAAGGCAAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTCGGATTGTGAAATGGTAGGAATAATCCTTG
AACAAAGGAAAATCTTTAAAGAACAGAAGGCACAACTCAAATGTGAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAA
AAAAAAA
AAAAA

FIGURE 122

MNSSKSSETQCTERGCFSQMFQFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCCTCGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGCTCGGCTGCTGACTTCTTCCTGCTGCTGCTTTCAGGGGCTGCCTGATAGGGGCTGTAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCCTGCATCATTACGGATTGCG
AGACAAGTACCCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAAACAACACATATGTGTTTTGACAACAAA
TTCAGGGAGACTTGGCGGCTGTCAGAAATACTGGGAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTGTTGCTGAAATGACCGCAAGGAAATTGATGAGATTGATGAGTTAA
CTGTGCAAGTGAAGCCAGTGCACCCCTGCTGTAGAGTGCAGGCTGTACAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTCTTCCACCTAAACTCTGAAACAGCAGCTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCAATTGCTTCAATGACCGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATTGGCGGAATTATTGGGGGGTTCTGGTGTCTGCTGTACTGGCCCTGA
TCACGTTGGGATCTGCTGTGCATACAGACGTGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACACAGATGGAGTTAACATCCTGCAACTGACAGGAGGGCAGCTCAGACACAAGTCATGTTG
TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCAGCAGTCACATCCCTGCTAGAAACTCCTGCTCAA
GGCAGCGAGAGCTGATGCACTGGACAGAGCTAGACACTCATTAGAAGCTTTCCTCAAGATGGACCCGGTAATATAACCAA
CTACTCTTCTTAACAAAGCCACATGAATAGAAGAATTTCCTCAAGATGGACCCGGTAATATAACCAA
GGAAGCGGAAACTGGGTGGCTTCACTGAGTTGGGTTCTTAACCTGTTCTGGCTGATTCCCGATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACGCCCCGTGCTGGCCCTGTAAGGCCAGCATGTTACCAACTGGTCGT
CAGCAGCCACGACAGCACCAGTGGAGATGGCAGGGTGGACAGCACCAGCAGCGCATCCGGCGGGAACCA
GAAAAGGCTTCTTACACAGCAGCTTACTTCATGGCCCCACAGACACCACCGCAGTTCTTAAAGGCTCTGC
TGATGGTGTGCACTGTCATTGTGGAGAAGCTTTGGATCAGCATTTGTAACAAACACAAAATCAGGAAG
GTAAATTGGTTGCTGGAAGAGGGATCTTGCCTGAGGAACCTGCTTGTCCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTTCGTCTTAAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGTGTTATTGTTATAAAATT
TACATCTAAATTGGCTAAGGATGTTATTGATTATTGAAAAGAAAATTCTATTAAACTGTAATATATTGT
CATACATGTTAAATAACCTATTGTTAAAAAGTCAACTTAAGGTTAGAAGTCTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTGTTACCAAGGAATTCTCTCATGGAAGTTACTGTGATGTTCTTCT
CACACAAGTTTAGCCTTTCAAAAGGAACCTCATACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCAGTTAACGCAATGTTGAAATCAGTTGCTACTCTTCAAAAGAAACCTCTCAGGTTAGCTTGAAC
GCCTCTCTGAGATGACTAGGACAGTGTACCCAGAGGCCACCCAGAAGGCCCTGAGATGACATACACAGATG
CCAGTCAGCTCTGGGGTTGCCAGGCCAGGCCCTGGCTAGTGTACCCAGAGGCCACCCAGAAGGCCCTGAGATG
GCCATCCTGGGCCCTGGCAGTGGCTGTGCCCCAGTGGCTTACTCAGTGGCCCTTGCTCATCCAGCACAGC
TCTCAGGTGGGACTGCAGGGACACTGGGTCTCCATGCTAGCCTGCTGCTGCTGCTGCTGCTGCT
TTTGGTTATGGATGGCTCACAAATAGGGCCCCAATGCTATTGTTTTAAGTTGTTAATTGTT
AAGATTGCTAAGGCCAAAGGAATTGCAAAATCAAGTCTGCAAGTACAATAACATTAAAAGAAAATGGAT
CCCACTGTTCTTGCACAGAGAAAGCACCCAGACGCCACAGGCTCTGCGATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAGGTGGAGCAGGCCAGGTGAAAGGCCCTGGGGAGGAAAG
TGAAACGCTGAATCAAAGCAGTTCTAATTGACTTAAATTTCATCCGGAGACACTGCTCCATT
TGTGGGGGACATTAGCAACATCACTCAGAAGCCTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGAACAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTCCTGGA
GAATGGCTCTCACTACTCACCTGCTTTCAGCTTCACTGCTTGGGTTTTTATACATTGACAGCTTTTT
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCCTGAGGCCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCCTGGGTCTGCTGCATGGCATCTGGATGCTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTCACTGCTCCAGCCTCCT
TCTTGGTTGTCATAGTGTAGGGTAGCCTTATTGCCCCCTTCTTATACCCCTAAACCTCTACACTAGTGC
TGGGAACCAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTGTTGTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACAGGAGGCTGATTCT
GCCTTGGATGGATGTTGCTGACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVLAVALALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267